

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model
Run on: April 3, 2004, 12:38:43 ; Search time 5583 Seconds
(without alignments)
10449.530 Million cell updates/sec
Title: US-09-989-724-386
Perfect score: 1346
Sequence: 1 gaaagaatgttgctgct.....aaaaa 1346
Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
Searched: 3470272 segs, 21671516995 residues
Total number of hits satisfying chosen parameters: 6940544
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:

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- 8: gb_pl.*
- 9: gb_pr.*
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- 11: gb_sts.*
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- 38: em_sy.*
- 39: em_htgo_hum.*
- 40: em_htgo_mus.*
- 41: em_htgo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1346	100.0	1346	6	AR252633	AR252633 Sequence
2	1346	100.0	1346	6	AX403499	AX403499 Sequence
3	1346	100.0	1346	6	AX464348	AX464348 Sequence
4	1346	100.0	1346	9	AY359060	AY359060 Homo sapi
5	1328.6	98.7	1605	9	BC014317	BC014317 Homo sapi
6	1325.4	98.5	1377	9	BC050606	BC050606 Homo sapi
7	1325.4	98.5	1440	9	BC015099	BC015099 Homo sapi
8	1324.6	98.4	1447	6	BD205644	BD205644 97 human
9	1321.8	98.2	1401	6	BD083420	BD083420 Secreted
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12	1305	97.0	1356	6	BD135300	BD135300 110 human
13	845.2	62.8	862	6	BD270445	BD270445 Genes ass
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16	799.4	59.4	848	6	AR340701	AR340701 Sequence
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18	799.4	59.4	848	6	AX884142	AX884142 Sequence
19	799.4	59.4	848	6	BD023757	BD023757 Sequence
20	799.4	59.4	848	6	BD073618	BD073618 5'EST of
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31	793.4	58.9	159446	9	AC003669	AC003669 Homo sapi
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35	589.8	43.8	1262	10	AF178085	AF178085 Mus muscu
36	539.6	40.1	1181	10	AF178086	AF178086 Rattus no
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38	405	30.1	462	6	BD058424	BD058424 Secreted
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43	157.4	11.7	226820	2	AC118872	AC118872 Rattus no
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45	125.6	9.3	2415	6	AX047764	AX047764 Sequence

ALIGNMENTS

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LOCUS	Sequence	386 from patent US 6478825.				
DEFINITION	AR252633					
ACCESSION	AR252633.1	GI:27300541				
VERSION	Unknown.					
KEYWORDS	Unknown.					
SOURCE	Unclassified.					
ORGANISM	1 (bases 1 to 1346)					
REFERENCE	Winterbottom,J.M., Shimp,L., Boyce,T.M. and Kaes,D.					
AUTHORS	Implant, method of making same and use of the implant for the					
TITLE	treatment of bone defects					
JOURNAL	Patent: US 6478825-A 386 12-NOV-2002;					

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Qy	61	CCAGGTGCAGAAAAATGCTTTTAAAGTGAGACTTAGTATCAGAAACAGCTCTGGGAGATAAA	120
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Qy	121	GCATATGCTGGGATACCAATGAAGATPACCTCTTCAAAGCGATGGTAGCTTCTCCATG	180
Db	121	GCATATGCTGGGATACCAATGAAGATPACCTCTTCAAAGCGATGGTAGCTTCTCCATG	180
Qy	181	AGAAAGTTCCTCAACAGAGAAAGCAACAGAAATTTCCCATGTCTTCTGCAATGTAAACC	240
Db	181	AGAAAGTTCCTCAACAGAGAAAGCAACAGAAATTTCCCATGTCTTCTGCAATGTAAACC	240
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Db	241	CAGAGGTATCATTTCTGGTTTGTGGTTACAGACCCCTTCAAAAAATCACACCCCTTCTGTCT	300
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Db	301	GTTGAGGTGCAATCAGCCATAAGAAATGAACAGAAACCGGATCAACCAATGCTCTTTCTTA	360
Qy	361	AATGACCAAACTCTGGAATTTTAAAAATCCCTTCCACACTTGCACCCCATGGACCCA	420
Db	361	AATGACCAAACTCTGGAATTTTAAAAATCCCTTCCACACTTGCACCCCATGGACCCA	420
Qy	421	TCTGTGCCCATCTGGATTATATATTTTGGTGTGATATTTTGCATCATCATAGTTGCAATT	480
Db	421	TCTGTGCCCATCTGGATTATATATTTTGGTGTGATATTTTGCATCATCATAGTTGCAATT	480
Qy	481	GCACTACTGATTTTATCAGGGATCTGGCAACCTAGAAGAAAGCAACCAACCATCTGAA	540
Db	481	GCACTACTGATTTTATCAGGGATCTGGCAACCTAGAAGAAAGCAACCAACCATCTGAA	540
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Db	541	GTGGATGACGCTGAAGATAAGTGTGAAACATGATCACAAATGAAGATGGCATCCCTCT	600
Qy	601	GATCCCTTGGACATGAAGGGGGCATATTAATGATGCCCTTCATGACAGAGGATGAGAGGC	660
Db	601	GATCCCTTGGACATGAAGGGGGCATATTAATGATGCCCTTCATGACAGAGGATGAGAGGC	660
Qy	661	TCACCCCTCTCTGAAGGGCTGTGTTCTGCTTCTCAAGAAATTAACATTTGTTTCTGT	720
Db	661	TCACCCCTCTCTGAAGGGCTGTGTTCTGCTTCTCAAGAAATTAACATTTGTTTCTGT	720
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Db	901	TAGTGATATAATGTGGTCATGTGGTATTTGTAGTTATTTGATTTTAAAGCAATTTTAAATA	960

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RESULT 2

AX403499

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

source

ORIGIN

Query Match

Best Local Similarity

Matches 1346; Conservative

0; Mismatches

0; Indels

0; Gaps

0;

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AX403499

Sequence 386 from Patent WO0073454.

AX403499

AX403499.1

GI:21436987

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1

Ashkenazi, A.J., Baker, K.P., Botstein, D., Desnovers, L., Eaton, D., Ferrara, N., Gerber, H., Gerritsen, M., Goddard, A., Godowski, P., Grimaldi, C.J., Gurney, A.L., Kljavin, I., Napier, M.A., Pan, J., Paoni, N.F., Roy, M., Stewart, T.A., Tumas, D., Watanabe, C.K., Williams, P., Wood, W.I. and Zhang, Z.

Secreted and transmembrane polypeptides and nucleic acids encoding the same

Patent: WO 0073454-A 386 07-DEC-2000;

Genentech Inc. (US)

Location/Qualifiers

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/mol_type="unassigned DNA"

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RESULT 3
AX464348
LOCUS AX464348 1346 bp DNA linear PAT 16-JUL-2002
DEFINITION Sequence 481 from Patent WO0140466.
ACCESSION AX464348
VERSION AX464348.1 GI:21899190
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1
AUTHORS Baker, K.P., Beresini, M., Deforge, L., Desnoyers, L., Filvaroff, E.,
Gao, W.Q., Gerritsen, M.E., Goddard, A., Godowski, P.J., Gurney, A.L.,
Sherwood, S., Smith, V., Stewart, T.A., Tumas, D., Watanabe, C.K.,
Wood, W.L. and Zhang, Z.
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding
JOURNAL same
PATENT: WO 0140466-A 481 07-JUN-2001;
Genentech Inc. (US)
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Best Local Similarity 100.0%; Pred. No. 2e-266;
Matches 1346; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DEFINITION Homo sapiens clone DNA61873 NX-17 (UNQ678) mRNA, complete cds.
ACCESSION AY359060
VERSION AY359060.1 GI:37183237
KEYWORDS FLI CDNA.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1346)
AUTHORS Clark,H.F., Gurney,A.L., Abaya,E., Baker,K., Baldwin,D., Brush,J.,
```

Chen,J., Chow,B., Chui,C., Crowley,C., Currell,B., Deuel,B., Dowd,P., Eaton,D., Foster,J., Grimaldi,C., Gu,Q., Hass,P.E., Heldens,S., Huang,A., Kim,H.S., Klimowski,L., Jin,Y., Johnson,S., Lee,J., Lewis,L., Liao,D., Mark,M., Robbie,B., Sanchez,C., Schoenfeld,J., Seehagiri,S., Simmons,L., Singh,J., Smith,V., Stinson,J., Vagts,A., Vandlen,R., Watanabe,C., Wieand,D., Woods,K., Xie,M.H., Yansura,D., Yi,S., Yu,G., Yuan,J., Zhang,M., Zhang,Z., Goddard,A., Wood,W.I. and Godowski,P.
The Secreted Protein Discovery Initiative (SPDI), a Large-Scale Effort to Identify Novel Human Secreted and Transmembrane Proteins: A Bioinformatics Assessment
Genome Res. 13 (10), 2265-2270 (2003)
12975309
2 (bases 1 to 1346)
Clark,H.F.
Direct Submission
Submitted (01-AUG-2003) Department of Bioinformatics, Genentech, Inc., 1 DNA Way, South San Francisco, CA 94080, USA
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RESULT 5

BC014317

LOCUS BC014317 1605 bp mRNA linear PRI 04-OCT-2003

DEFINITION Homo sapiens kidney-specific membrane protein, mRNA (cdna clone MGC:22707 IMAGE:4048217), complete cds.

ACCESSION BC014317

VERSION BC014317.1 GI:15680012

KEYWORDS MGC.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE
AUTHORS

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

1 (bases 1 to 1605)

Strausberg, R.L., Feingold, B.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, P.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diachenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.P., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Ustin, T.B., Toshikiyuki, S., Carninci, P., Frange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Pahey, J., Helton, E., Kettelman, M., Madan, A., Rodrigues, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E., Schnerch, A., Schein, J.E., Jones, S.J., and Marra, M.A.

TITLE

human and mouse cDNA sequences

Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

JOURNAL

MEDLINE

PUBMED

12477932

REFERENCE

AUTHORS

TITLE

JOURNAL

REMARK

COMMENT

NIH-MGC Project URL: <http://mgc.nci.nih.gov>

Contact: MGC help desk

Email: cgapbs-remail.nih.gov

Tissue Procurement: ATCC

cdna Library Preparation: CLONTECH Laboratories, Inc.

cdna Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Institute for Systems Biology

<http://www.systemsbio.org>

contact: amadnan@systemsbiology.org

Anup Madan, Jessica Pahey, Erin Helton, Mark Kettelman, Anuradha

Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>

Series: IRAL Plate: 31 Row: n Column: 3.

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RESULT 6
BC050606
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

BC050606
Homo sapiens kidney-specific membrane protein, mRNA (cDNA clone
MGC:6059 IMAGE:5183554), complete cds.
BC050606
BC050606.1 GI:30047080
MGC.
Homo sapiens (human)
Homo sapiens

REFERENCE
AUTHORS

1 (bases 1 to 1377)
Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Udén, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, E., Kettner, M., Madan, A., Rodriguez, S.,
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Krzywinski, M.I., Skalek, U., Smailus, D.E.,
Schnierch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS
TITLE
JOURNAL

2 (bases 1 to 1377)
Strausberg, R.
Direct Submission
Submitted (08-APR-2003) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
NIH-MGC Project URL: <http://mgc.nci.nih.gov>
Contact: MGC help desk
Email: cgapbs-re@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.

REMARK
COMMENT

cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 94305
Web site: <http://www-shgc.stanford.edu>
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,
R. M.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Series: IRAC Plate: 110 Row: c Column: 4
This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA gi: 21361864.

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gene

CDS

ORIGIN

Query Match 98.5%; Score 1325.4; DB 9; Length 1377;
Best Local Similarity 99.5%; Pred. No. 3.5e-262;
Matches 1340; Conservative 0; Mismatches 6; Indels 1; Gaps 1;

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RESULT 7

BC015099

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

BC015099
Homo sapiens kidney-specific membrane protein, mRNA (cDNA clone
MGC:2827 IMAGE:3829035), complete cds.
BC015099
BC015099.1 GI:15929328
MGC.

SOURCE ORGANISM
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 1440)
Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, E., Kettelman, M., Madan, A., Rodriguez, S.,
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.B.,
Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
22388257
12477932
2 (bases 1 to 1440)
Strausberg, R.
Direct Submission
Submitted (01-OCT-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
NIH-MGC Project URL: <http://mgc.nci.nih.gov>
Contact: MGC help desk
Email: cgabbs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Institute for Systems Biology
<http://www.systemsbio.org>
contact: amadan@systemsbiology.org
Anup Madan, Jessica Fahey, Erin Helton, Mark Kettelman, Anuradha
Madan, Stephanie Rodriguez, Amy Sanchez and Michelle Whiting
Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
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Best Local Similarity 99.5%; Pred. No. 3.4e-262;
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RESULT 8
BD205644
LOCUS BD205644
DEFINITION 97 human secreted proteins.
ACCESSION BD205644
VERSION BD205644.1 GI:33015414
KEYWORDS JP 2002533058-A/21.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1447)
AUTHORS Ruben,S.M., Florence,K., Ni,J., Rosen,C.A., Carter,K.C.,
Moore,P.A., Olsen,H.S., Shi,Y., Young,P.E., Wei,F.F., Brewer,L.A.,
Soppet,D.R., Lafleur,D.W., Endress,G.A. and Ebner,R.
97 human secreted proteins
Patent: JP 2002533058-A 21 08-OCT-2002;
HUMAN GENOME SCIENCES INC
COMMENT OS Homo sapiens (human)
PN JP 2002533058-A/21
PD 08-OCT-2002
PF 06-MAY-1999 JP 2000548451
PR 12-MAY-1998 US 60/085093,12-MAY-1998 US 60/085094 PR
12-MAY-1998 US 60/085105,12-MAY-1998 US 60/085180 PR
18-MAY-1998 US 60/085927,18-MAY-1998 US 60/085906 PR
18-MAY-1998 US 60/085924,18-MAY-1998 US 60/085922 PR
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18-MAY-1998 US 60/085925,18-MAY-1998 US 60/085928 PR
PI STEVEN M RUBEN, KIMBERLY FLORENCE, JIAN NI, CRAIG A ROSEN, KENNETH
C CARTER,
PI PAUL A MOORE, HENRIK S OLSEN, YANGGU SHI, PAUL E YOUNG, PING FEI
PI WEI,
PI LAURIE A BREWER, DANIEL R SOPPET, DAVID W LAPLEUR, GREGORY A PI
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PI REINHARD EBNER
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DEFINITION
ACCESSION BD083420
VERSION BD083420.1 GI:22629030
KEYWORDS JP 2001523950-A/2.
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 1401)
AUTHORS Jacobs,K., McCooy,J.M., Lavallie,E.R., Racie,L.A., Merberg,D.,
Treacy,M., Spaulding,V. and Agostino,M.J.
TITLE Secreted proteins and polynucleotides encoding them
JOURNAL Patent: JP 2001523950-A 2 27-NOV-2001;
GENETICS INSTITUTE INC
COMMENT PN JP 2001523950-A/2
PD 27-NOV-2001
PF 23-JAN-1998 JP 1998532177
PR 24-JAN-1997 US 08/788789
PI KENNETH JACOBS,JOHN M MCCOY,EDWARD R LAVALLIE,LISA A RACIE, PI
DAVID MERBERG,
PI MAURICE TREACY,VIKKI SPAULDING,MICHAEL J AGOSTINO PC
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RESULT 10

AX083392

LOCUS AX083392 1347 bp DNA linear PAT 28-FEB-2001

DEFINITION Sequence 84 from Patent WO0112660.

ACCESSION AX083392

VERSION AX083392.1 GI:13185232

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1

AUTHORS Kato,S. and Kimura,T.

TITLE Human proteins having hydrophobic domains and dnas encoding these proteins

JOURNAL Patent: WO 0112660-A 84 22-FEB-2001;

FEATURES

source 1. .1347

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26. .694

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LTPL"

ORIGIN

Query Match 97.3%; Score 1309.4; DB 6; Length 1347;

Best Local Similarity 99.8%; Pred. No. 6.8e-259;

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Db 140 GCATATGCCTGGGATACCAATGAAGAATACCTCTTCAAGCGATGGTAGCTTTCTCCATG 199

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Db 1340 TGA 1342

RESULT 11
AF229179 LOCUS AF229179 1345 bp mRNA linear PRI 05-APR-2002
DEFINITION Homo sapiens collectrin mRNA, complete cds.
ACCESSION AF229179
VERSION AF229179.1 GI:9957753
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1345)
AUTHORS Zhang,H., Wada,J., Hida,K., Tsuchiyama,Y., Hiragushi,K.,
Shikata,K., Wang,H., Lin,S., Kanwar,Y.S. and Makino,H.
TITLE Collectrin, a collecting duct-specific transmembrane glycoprotein,
is a novel homolog of ACE2 and is developmentally regulated in
embryonic kidneys
J. Biol. Chem. 276 (20), 17132-17139 (2001)
MEDLINE 21264468
PubMed 11278314
REFERENCE 2 (bases 1 to 1345)
AUTHORS Zhang,H., Wada,J. and Makino,H.
TITLE Human kidney specific membrane protein (NX-17)
JOURNAL Unpublished
REFERENCE 3 (bases 1 to 1345)
AUTHORS Zhang,H., Wada,J. and Makino,H.
TITLE Direct Submission
JOURNAL Submitted (28-JAN-2000) Department of Medicine III, Okayama
University Medical School, 2-5-1 Shikata-cho, Okayama 700-8558,
Japan
FEATURES
source Location/Qualifiers
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ORIGIN
Query Match 97.2%; Score 1307.8; DB 9; Length 1345;
Best Local Similarity 99.8%; Pred. No. 1.4e-258;
Matches 1320; Conservative 0; Mismatches 2; Indels 1; Gaps 1;
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Db 1338 TGA 1340

RESULT 12

BD135300

LOCUS

DEFINITION

ACCESSION

BD135300

VERSION

BD135300.1 GI:23230245

KEYWORDS

JP 2002508167-A/51.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1356)

Moore,P.A., Ruben,S.M., Carter,K.C., Shi,Y., Rosen,C.A., Soppet,D.R., Caou,H., Wei,Y.F., Florence,K., Duan,R.D., Florence,C., Greene,J.M., Feng,P., Ferrie,A.M., Yu,G.L., Janat,F. and Ni,J.

110 human secretory proteins

Patent: JP 2002508167-A 51 19-MAR-2002;

HUMAN GENOME SCIENCES INC

OS Homo sapiens (human)

PN JP 2002508167-A/51

PD 19-MAR-2002

PF 17-DEC-1998 JP 2000539040

PR 18-DEC-1997 US 60/070 923,18-DEC-1997 US 60/068 007 PR

18-DEC-1997 US 60/068 057,18-DEC-1997 US 60/068 006 PR

18-DEC-1997 US 60/068 008,18-DEC-1997 US 60/068 054 PR

18-DEC-1997 US 60/068 064,18-DEC-1997 US 60/068 053 PR

19-DEC-1997 US 60/068 169,19-DEC-1997 US 60/068 368 PR

19-DEC-1997 US 60/068 367,19-DEC-1997 US 60/068 369 PR

19-DEC-1997 US 60/068 365

PI PAUL A MOORE,STEVEN M RUBEN,KENNETH C CARTER,YANGGU SHI,CRAIG PI A ROSEN,

PI DANIEL R SOPPET,HARA CAOU,YING FEI WEI,KIMBERLY FLORENCE, PI ROSANNE D DUAN,

PI CHARLES FLORENCE,JOHN M GREENE,PING FENG,ANN M FERRIE,GUO PI LIANG YU,

PI FORD JANAT,JIAN NI

PC C12N15/09,A61K38/00,A61K48/00,A61P9/00,A61P9/10,A61P15/00, PC A61P25/00,

PC A61P25/02,A61P25/14,A61P25/16,A61P25/18,A61P25/22,A61P25/24, PC A61P25/28,

PC A61P29/00,C07K14/47,C07K16/18,C12N1/15,C12N1/19,C12N1/21,C12N5/ PC 10,

PC C12P21/02,C12Q1/68,G01N33/15,G01N33/50,G01N33/53,C12N15/00, PC A61K37/02,

PC C12N5/00

CC n equals a,t,g, or c

FH Key Location/Qualifiers

FT source 1..1356 /organism='Homo sapiens {human}'.

FT Location/Qualifiers

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FEATURES

source

1..1356

ORIGIN

Query Match 97.0%; Score 1305; DB 6; Length 1356;

Best Local Similarity 99.0%; Pred. No. 5.4e-258;

Matches 1333; Conservative 0; Mismatches 11; Indels 2; Gaps 2;

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Qy 61 CCAGGTGCAGAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAA 120

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RESULT 13
BD270445
LOCUS BD270445 862 bp DNA linear PAT 17-JUL-2003
DEFINITION Genes associated with diseases of the kidney.
ACCESSION BD270445
VERSION BD270445.1 GI:33080213
KEYWORDS JP 2002541787-A/6.

SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 862)
AUTHORS Walker,M.G., Volkmut,W., Klingler,T.M., Azimzai,Y. and Yue,H.
TITLE Genes associated with diseases of the kidney
JOURNAL Patent: JP 2002541787-A 6 10-DEC-2002;
INCYTE PHARMACEUTICALS INC

COMMENT OS Homo sapiens (human)
PN JP 2002541787-A/6
PD 10-DEC-2002
PF 28-MAR-2000 JP 2000611563
PR 09-APR-1999 US 09/289349
PI MICHAEL G WALKER,WAYNE VOLKSMUTH,TOD M KLINGLER,YALDA AZIMZAI,
PI HENRY YUE
PC C12N15/09,A61K31/7115,A61K31/7125,A61K35/76,A61K38/00,A61K39/
PC 395,
PC A61K39/395,A61K39/395,A61K48/00,A61P5/38,A61P9/12,A61P13/04,
PC A61P13/12,
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DEFINITION Sequence 27 from patent US 6312922.
ACCESSION AR177334
VERSION AR177334.1 GI:17919689
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 848)
AUTHORS Edwards,J.-B.Dumas.Milne., Duclert,A. and Bougueleret,L.
TITLE Complementary DNAs
JOURNAL Patent: US 6312922-A 27 06-NOV-2001;
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DEFINITION 5' ESTs for secreted proteins expressed in various tissues.
ACCESSION BD247957
VERSION BD247957.1 GI:33057727
KEYWORDS JP 2002525024-A/22.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 848)
AUTHORS Edwards,J.B.D.M., Duclert,A. and Lacroix,B.
TITLE 5' ESTs for secreted proteins expressed in various tissues
JOURNAL Patent: JP 2002525024-A 22 13-AUG-2002;
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COMMENT OS Homo sapiens (human)
PN JP 2002525024-A/22
PD 13-AUG-2002
PF 31-JUL-1998 JP 2000505294
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LACROIX
PC C12N15/09,C12N15/09,C07K14/47,C12M1/00,C12P21/02,C12N15/00, PC
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CC Von Heijne matrix
CC score 10.7
CC seq LMLFFLVTAIHA/BL
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Best Local Similarity 98.8%; Pred. No. 4.6e-154;
Matches 809; Conservative 6; Mismatches 3; Indels 1; Gaps 1;

QY 1 GAAAGAAATGTTGTGGCTGCTCTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAA 60
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DT 05-APR-2000 (first entry)
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KW Membrane-bound polypeptide; PRO polypeptide; LDL receptor; TIB ligand;
KW pharmaceutical; receptor immunoadhesin; gene mapping; ss.
XX
OS Homo sapiens.
XX
PN WO9963088-A2.
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PD 09-DEC-1999.
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PF 02-JUN-1999; 99WO-US012252.
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PR 02-JUN-1998; 98US-0087607P.
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PR 19-AUG-1998; 98US-0097141P.
PR 20-AUG-1998; 98US-0097218P.
PR 24-AUG-1998; 98US-0097661P.
PR 26-AUG-1998; 98US-0097951P.
PR 26-AUG-1998; 98US-0097952P.
PR 26-AUG-1998; 98US-0097954P.
PR 26-AUG-1998; 98US-0097955P.
PR 26-AUG-1998; 98US-0097971P.
PR 26-AUG-1998; 98US-0097974P.
PR 26-AUG-1998; 98US-0097978P.
PR 26-AUG-1998; 98US-0097979P.
PR 26-AUG-1998; 98US-0097986P.
PR 26-AUG-1998; 98US-0098014P.
PR 31-AUG-1998; 98US-0098525P.
PR 16-SEP-1998; 98US-0100634P.
PR 12-JAN-1999; 99US-0115565P.
XX
PA (GETH) GENENTECH INC.
XX
PI Baker K, Chen J, Goddard A, Gurney AL, Smith V, Watanabe CK;
PI Wood WI, Yuan J;
XX
DR WPI; 2000-072883/06.
DR P-PSDB; AAY66751.
XX
PT Membrane-bound proteins and related nucleotide sequences.
XX
PS Claim 2; Fig 277; 822pp; English.
XX
CC The invention provides membrane-bound PRO polypeptides and
CC polynucleotides encoding them. The PRO sequences of the invention were
CC identified based on extracellular domain homology screening. The PRO
CC sequences have homology with proteins including LDL receptors, TIE
CC ligands and various enzymes. The membrane-bound proteins and receptor
CC molecules are useful as pharmaceutical and diagnostic agents. Receptor
CC immunoadhesins, for instance, can be used as therapeutic agents to block
CC receptor-ligand interactions. The membrane-bound proteins can also be
CC employed for screening of potential peptide or small molecule inhibitors
CC of the relevant receptor/ligand interaction. The PRO encoding sequences
CC are useful as hybridization probes, in chromosome and gene mapping and in
CC the generation of antisense RNA and DNA. PRO nucleic acid sequences will
CC also be useful for the preparation of PRO polypeptides, especially by
CC recombinant techniques
XX
SQ Sequence 1346 BP; 457 A; 245 C; 237 G; 407 T; 0 U; 0 Other;

Query Match 100.0%; Score 1346; DB 3; Length 1346;
Best Local Similarity 100.0%; Pred. No. 1.6e-262;
Matches 1346; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAAGAATGTTGGCTGCTCTTTTCTGGTGACTGCCATTGCTGAACCTGTGCAA 60

Db 1 GAAAGAAATGTTGGTCTCTCTTTTCTGGTACTGCCATTCTGCTGAATCTGTCAA 60
Qy 61 CCAGGTGCAGAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAA 120
Db 61 CCAGGTGCAGAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAA 120
Qy 121 GCATATGCTGGGATACCAATGAAGAATACCTCTTCAAGCGATGGTAGCTTTCTCCATG 180
Db 121 GCATATGCTGGGATACCAATGAAGAATACCTCTTCAAGCGATGGTAGCTTTCTCCATG 180
Qy 181 AGAAAAGTTCCCAACAGAGAACAGAAAATTTCCCATGTCTTACTTTGCAATGTAACC 240
Db 181 AGAAAAGTTCCCAACAGAGAACAGAAAATTTCCCATGTCTTACTTTGCAATGTAACC 240
Qy 241 CAGAGGGTATCATCTGTTTGTGGTTACAGACCTTCAAAAATCAGACCCCTTCTGCT 300
Db 241 CAGAGGGTATCATCTGTTTGTGGTTACAGACCTTCAAAAATCAGACCCCTTCTGCT 300
Qy 301 GTTGAGGTGCAATCAGCCATAGCAATGAACAAGACCGGATCAACAATGCCTTCTTCTA 360
Db 301 GTTGAGGTGCAATCAGCCATAGCAATGAACAAGACCGGATCAACAATGCCTTCTTCTA 360
Qy 361 AATGACCAAACCTGGAATTTTAAATAATCCCTTCCACACTTGACACCCATGACCCCA 420
Db 361 AATGACCAAACCTGGAATTTTAAATAATCCCTTCCACACTTGACACCCATGACCCCA 420
Qy 421 TCTGTGCCATCTGGATTAATATATTTGGTGTGATATTTTGGCATCATATGTTGCAATT 480
Db 421 TCTGTGCCATCTGGATTAATATATTTGGTGTGATATTTTGGCATCATATGTTGCAATT 480
Qy 481 GCACTACTGATTTTATCAGGGATCTGGCAACGCTAGAAGAAAGAAACAAAGAACCACTGAA 540
Db 481 GCACTACTGATTTTATCAGGGATCTGGCAACGCTAGAAGAAAGAAACAAAGAACCACTGAA 540
Qy 541 GTGGATGACGCTGAAGATAAGTGTGAAGAACATGATCAACAATGGAATGGCATCCCTCT 600
Db 541 GTGGATGACGCTGAAGATAAGTGTGAAGAACATGATCAACAATGGAATGGCATCCCTCT 600
Qy 601 GATCCCTTGACATGAAGGGGGCATATTAATGATGCTTCAAGAAATTAAGGATGAGAGGC 660
Db 601 GATCCCTTGACATGAAGGGGGCATATTAATGATGCTTCAAGAAATTAAGGATGAGAGGC 660
Qy 661 TCACCCCTCTCTGAAGGGCTGTTGTTCTGCTTCTCAAGAAATTAAGGATGAGAGGC 720
Db 661 TCACCCCTCTCTGAAGGGCTGTTGTTCTGCTTCTCAAGAAATTAAGGATGAGAGGC 720
Qy 721 GTGACTGCTGAGCATCTGAAATACCAAGAGCAGATCATATATTTTTCACCATCTT 780
Db 721 GTGACTGCTGAGCATCTGAAATACCAAGAGCAGATCATATATTTTTCACCATCTT 780
Qy 781 CTTTGTAAATAATTTGAATGCTTGAAGTGAAAGTGAAAGGCAATCAATATACCCACCAAC 840
Db 781 CTTTGTAAATAATTTGAATGCTTGAAGTGAAAGTGAAAGGCAATCAATATACCCACCAAC 840
Qy 841 ACCACTGAAATCATAAGCTATTACGACTCAAAATATTTCTAAATATTTTCTGACAGTA 900
Db 841 ACCACTGAAATCATAAGCTATTACGACTCAAAATATTTCTAAATATTTTCTGACAGTA 900
Qy 901 TAGTGATAAATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGAT 960
Db 901 TAGTGATAAATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGAT 960
Qy 961 AGATCAGGCATATGATATATTTTCACTTCAAGACCTAAGGAAAAATAAATTTTCCA 1020
Db 961 AGATCAGGCATATGATATATTTTCACTTCAAGACCTAAGGAAAAATAAATTTTCCA 1020
Qy 1021 GTGAGAAATACATATAATATGCTGATGAAATCATTTGAAATGGAATGATGATGATGATGAT 1080
Db 1021 GTGAGAAATACATATAATATGCTGATGAAATCATTTGAAATGGAATGATGATGATGATGAT 1080
Qy 1081 CTTATATCACTCTGTATATGACTAAGTAAACAAAGTGAGAAATTAATTTGTAATGGA 1140
Db 1081 CTTATATCACTCTGTATATGACTAAGTAAACAAAGTGAGAAATTAATTTGTAATGGA 1140

Db 1081 CTTATATCACTCTGTATATGACTAAGTAAACAAAGTGAGAAATTAATTTGTAATGGA 1140
Qy 1141 TGGATAAAAATGGAATTAATCTATATACAGGGTGGAATTTTATCCTGTTATCACACCAACA 1200
Db 1141 TGGATAAAAATGGAATTAATCTATATACAGGGTGGAATTTTATCCTGTTATCACACCAACA 1200
Qy 1201 GTTGATATATATTTTCTGAATATCAGCCCTTAATAGGACAAATTTCTATTTGTTGACCAAT 1260
Db 1201 GTTGATATATATTTTCTGAATATCAGCCCTTAATAGGACAAATTTCTATTTGTTGACCAAT 1260
Qy 1261 TCTACAAATTTGTAAGTCCAATCTGTGCTAACTTAATAAGTAAATATATCATCTCTTTT 1320
Db 1261 TCTACAAATTTGTAAGTCCAATCTGTGCTAACTTAATAAGTAAATATATCATCTCTTTT 1320
Qy 1321 AAAAAAATAAAAAAATAAAAAA 1346
Db 1321 AAAAAAATAAAAAAATAAAAAA 1346
RESULT 2
AAC58612
ID AAC58612 standard; cDNA; 1346 BP.
XX
AC AAC58612;
XX
DT 29-JAN-2001 (first entry)
XX
DE Human PRO1312 protein UNQ678 encoding cDNA SEQ ID NO:160.
XX
KW Human; immune related disease; diagnosis; antiinflammatory; cardiant;
KW dermatological; antiarthritic; antirheumatic; immunosuppressive;
KW haemostatic; antithyroid; antidiabetic; nootropic; neuroprotective;
KW antianaemic; hepatotropic; virucide; antipsoxiatic; antiallergic;
KW antiasthmatic; systemic lupus erythematosus; rheumatoid arthritis;
KW osteoarthritis; spondyloarthropathy; systemic sclerosis; sarcoidosis;
KW idiopathic inflammatory myopathy; Sjogren's syndrome; thyroiditis;
KW systemic vasculitis; autoimmune haemolytic anaemia; diabetes mellitus;
KW autoimmune thrombocytopaenia; immune-mediated renal disease;
KW demyelinating disease; hepatobiliary disease; Whipple's disease;
KW inflammatory bowel disease; gluten-sensitive enteropathy;
KW autoimmune disease; immune-mediated skin disease; allergic disease;
KW immunological disease; transplantation associated disease;
KW graft rejection; graft-versus-host-disease; ss.
XX
OS Homo sapiens.
XX
PN WO200053758-A2.
XX
PD 14-SEP-2000.
XX
PP 02-MAR-2000; 2000WO-US005841.
XX
PR 08-MAR-1999; 99WO-US005028.
PR 10-MAR-1999; 99US-0123618P.
PR 12-MAR-1999; 99US-0123957P.
PR 23-MAR-1999; 99US-0125775P.
PR 12-APR-1999; 99US-0128849P.
PR 20-APR-1999; 99WO-US008615.
PR 28-APR-1999; 99US-0131445P.
PR 04-MAY-1999; 99US-0132371P.
PR 14-MAY-1999; 99US-0134287P.
PR 02-JUN-1999; 99WO-US012252.
PR 23-JUN-1999; 99US-0141037P.
PR 20-JUL-1999; 99US-0144758P.
PR 26-JUL-1999; 99US-0145698P.
PR 28-JUL-1999; 99US-0146222P.
PR 01-SEP-1999; 99WO-US020111.
PR 08-SEP-1999; 99WO-US020594.
PR 13-SEP-1999; 99WO-US020944.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 05-OCT-1999; 99WO-US023089.
PR 29-OCT-1999; 99US-0162506P.

PR 29-NOV-1999; 99WO-US028214.
PR 30-NOV-1999; 99WO-US028313.
PR 30-NOV-1999; 99WO-US028409.
PR 01-DEC-1999; 99WO-US028301.
PR 01-DEC-1999; 99WO-US028634.
PR 02-DEC-1999; 99WO-US028551.
PR 02-DEC-1999; 99WO-US028564.
PR 02-DEC-1999; 99WO-US028565.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030999.
PR 30-DEC-1999; 99WO-US031274.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000277.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 18-FEB-2000; 2000WO-US004342.
PR 22-FEB-2000; 2000WO-US004414.

XX (GETH) GENENTECH INC.

PI Ashkenazi AJ, Baker KP, Goddard A, Gurney AL, Hebert C, Henzel W;
PI Kabakoff RC, Lu Y, Pan J, Pennica D, Shelton DL, Smith V;
PI Stewart TA, Tumas D, Watanabe CK, Wood WI, Yan M;

XX WPI; 2000-572271/53.
DR P-PSDB; AAB33447.

XX Sixty four PRO polypeptides, useful in the diagnosis and treatment of
PT immune related disorders, e.g. systemic lupus erythematosus, rheumatoid
PT arthritis, osteoarthritis, thyroiditis and diabetes mellitus.

XX Claim 23; Fig 67; 309pp; English.

CC The present invention describes sixty four human PRO proteins which can
CC be used in the treatment of immune related diseases. The human PRO
CC proteins, anti-PRO antibodies, agonists and antagonists are useful for
CC treating and diagnosing immune related disorders. The disorders are
CC selected from systemic lupus erythematosus, rheumatoid arthritis,
CC osteoarthritis, juvenile chronic arthritis, spondyloarthropathies,
CC systemic sclerosis, idiopathic inflammatory myopathies, Sjogren's
CC syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic
CC anaemia, autoimmune thrombocytopenia, thyroiditis, diabetes mellitus,
CC immune-mediated renal disease, demyelinating diseases of the central and
CC peripheral nervous systems, hepatobiliary diseases, inflammatory bowel
CC disease, gluten-sensitive enteropathy and Whipple's disease, autoimmune
CC or immune-mediated skin diseases, allergic diseases, immunological
CC diseases of the lung, and transplantation associated diseases including
CC graft rejection and graft-versus-host-disease. AAC58397 to AAC58578
CC represent PCR primers and hybridisation probes used in the isolation of
CC human PRO sequences. AAC58579 to AAC58642 and AAB33414 to AAB33477
CC represent human PRO polynucleotide and protein sequences given in the
CC exemplification of the present invention

XX SQ Sequence 1346 BP; 457 A; 245 C; 237 G; 407 T; 0 U; 0 Other;

Query Match 100.0%; Score 1346; DB 3; Length 1346;
Best Local Similarity 100.0%; Pred. No. 1.6e-262;
Matches 1346; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAAGATGTTGGCTGCTCTTTTCTGGTGACTGCCATTTCATGCTGAACCTCTGTCAA 60
DB |||||||
QY 61 CCAGGTGAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGAGATAAA 120
DB |||||||
QY 61 CCAGGTGAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGAGATAAA 120
QY 121 GCATATGCTGGGATACCAATGAAGATACCTCTTCAAGCGATGGTAGCTTCTCCATG 180
DB |||||||
QY 121 GCATATGCTGGGATACCAATGAAGATACCTCTTCAAGCGATGGTAGCTTCTCCATG 180
QY 181 AGAAAGTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACC 240

DB |||||||
181 AGAAAGTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACC 240
QY |||||||
241 CAGAGGGTATCATTTCTGGTTTGTGTTTACAGACCCCTTCAAAAAATCAGACCCCTTCTGCT 300
DB |||||||
241 CAGAGGGTATCATTTCTGGTTTGTGTTTACAGACCCCTTCAAAAAATCAGACCCCTTCTGCT 300
QY |||||||
301 GTTGAGGTGCAATCAGCCCATAGATGAACAAGACCGGATCAACAATGCTTCTTTCTA 360
DB |||||||
301 GTTGAGGTGCAATCAGCCCATAGATGAACAAGACCGGATCAACAATGCTTCTTTCTA 360
QY |||||||
361 AATGACCAAACTCTGGAATTTTAAATAATCCCTTCCACACTTGCACCAATGGACCCA 420
DB |||||||
361 AATGACCAAACTCTGGAATTTTAAATAATCCCTTCCACACTTGCACCAATGGACCCA 420
QY |||||||
421 TCTGTGCCCATCTCGAATTTATATTTGGTGTGATATTTTGCATCATATAGTTGCAATT 480
DB |||||||
421 TCTGTGCCCATCTCGAATTTATATTTGGTGTGATATTTTGCATCATATAGTTGCAATT 480
QY |||||||
481 GCACACTGATTTTATCAGGGATCTGGCAACGTTAGAGAAAGAAACCAATCTCTGAA 540
DB |||||||
481 GCACACTGATTTTATCAGGGATCTGGCAACGTTAGAGAAAGAAACCAATCTCTGAA 540
QY |||||||
541 GTGGATGACGCTGAAGATAAGTGTGAACAATGATGACAAATGGAATGGCATCCCTCT 600
DB |||||||
541 GTGGATGACGCTGAAGATAAGTGTGAACAATGATGACAAATGGAATGGCATCCCTCT 600
QY |||||||
601 GATCCCTGGACATGAAGGGGGCATATTAATGATGCTTCATGACAGAGGATGAGAGGC 660
DB |||||||
601 GATCCCTGGACATGAAGGGGGCATATTAATGATGCTTCATGACAGAGGATGAGAGGC 660
QY |||||||
661 TCACCCCTCTCTGAAGGGCTGTTGTTCTGCTTCTCAAGAAATTAACATTTGTTCTGT 720
DB |||||||
661 TCACCCCTCTCTGAAGGGCTGTTGTTCTGCTTCTCAAGAAATTAACATTTGTTCTGT 720
QY |||||||
721 GTGACTGTGAGCATCTGAAATACCAAGAGCAGATCATATATTTTGTTCACCATTTCT 780
DB |||||||
721 GTGACTGTGAGCATCTGAAATACCAAGAGCAGATCATATATTTTGTTCACCATTTCT 780
QY |||||||
781 CTTTTGTAATAAATTTGAAATGTGCTTGAAGTGAAGCAATCAATATATACCCCAAC 840
DB |||||||
781 CTTTTGTAATAAATTTGAAATGTGCTTGAAGTGAAGCAATCAATATATACCCCAAC 840
QY |||||||
841 ACCACTGAAATCATAAAGCTATTACAGACTCAAAATATTTCTAAATATTTTCTGACAGTA 900
DB |||||||
841 ACCACTGAAATCATAAAGCTATTACAGACTCAAAATATTTCTAAATATTTTCTGACAGTA 900
QY |||||||
901 TAGTGATAAATGTGTCATGTGGTATTTGTAGTTTAAAGCAATTTTAGAATA 960
DB |||||||
901 TAGTGATAAATGTGTCATGTGGTATTTGTAGTTTAAAGCAATTTTAGAATA 960
QY |||||||
961 AGATCAGGCATATGTATATATTTTCACTTCAAGACCTAAGGAAAAATAAATTTTCCA 1020
DB |||||||
961 AGATCAGGCATATGTATATATTTTCACTTCAAGACCTAAGGAAAAATAAATTTTCCA 1020
QY |||||||
1021 GTGGAGAAATACATATAATATGTTGTAGAAATCATTTGAAATGGATCCTTTTGTACGATCA 1080
DB |||||||
1021 GTGGAGAAATACATATAATATGTTGTAGAAATCATTTGAAATGGATCCTTTTGTACGATCA 1080
QY |||||||
1081 CTTATATCACTCTGTATATGACTAAGTAAACAAAGTGAAGTAATTTATGTAATGGA 1140
DB |||||||
1081 CTTATATCACTCTGTATATGACTAAGTAAACAAAGTGAAGTAATTTATGTAATGGA 1140
QY |||||||
1141 TGGATAAAATGGAATTTACTCATATACAGGGTGGAAATTTTCTCTGTTATCACACCAACA 1200
DB |||||||
1141 TGGATAAAATGGAATTTACTCATATACAGGGTGGAAATTTTCTCTGTTATCACACCAACA 1200
QY |||||||
1201 GTTGATTATATATTTTCTGAATATCAGCCCTTAATAGGCAATTTCTATTTGTGACCAAT 1260
DB |||||||
1201 GTTGATTATATATTTTCTGAATATCAGCCCTTAATAGGCAATTTCTATTTGTGACCAAT 1260
QY |||||||
1261 TCTACAATTTGTAAAAGTCCCAATCTGTGCTAACTTAATAAGTAATAATCATCTCTTTT 1320

Db 1261 TCTACAATTTGTAAAGTCCAATCTGTGCTAACTTAATAAAGTAATAATCAATCTCTTTT 1320
QY 1321 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1346
Db 1321 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1346

RESULT 3
AAA77680
ID AAA77680 standard; cDNA; 1346 BP.
XX
AC AAA77680;
XX
DT 07-NOV-2000 (first entry)
XX
DE Human PRO1312 cDNA sequence SEQ ID NO:213.
XX
KW Human; PRO; promotion; inhibition; angiogenesis; cardiovascularisation;
KW diagnosis; trauma; wound; cancer; atherosclerosis; cardiac hypertrophy;
KW angiogenic; proliferative; cardiant; cardiovascular; antiatherosclerotic;
KW cytotstatic; gene therapy; vaccine; ss.
OS Homo sapiens.
XX
PN WO200032221-A2.
XX
PD 08-JUN-2000.
XX
PF 30-NOV-1999; 99WO-US028313.
XX
PR 01-DEC-1998; 98WO-US025108.
PR 16-DEC-1998; 98US-0112850P.
PR 12-JAN-1999; 99US-0115554P.
PR 08-MAR-1999; 99WO-US005028.
PR 12-MAR-1999; 99US-0123957P.
PR 28-APR-1999; 99US-0131445P.
PR 14-MAY-1999; 99US-0134287P.
PR 02-JUN-1999; 99WO-US012252.
PR 23-JUN-1999; 99US-0141037P.
PR 20-JUL-1999; 99US-0144758P.
PR 26-JUL-1999; 99US-0145698P.
PR 01-SEP-1999; 99WO-US020111.
PR 08-SEP-1999; 99WO-US020594.
PR 13-SEP-1999; 99WO-US020944.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 05-OCT-1999; 99WO-US023089.
PR 29-OCT-1999; 99US-0162506P.
XX
PA (GETH) GENENTECH INC.
XX
PI Ashkenazi AJ, Baker KP, Ferrara N, Gerber H, Hillan KJ;
PI Goddard A, Godowski PJ, Gurney AL, Klein RD, Kuo SS, Paoni NF;
PI Smith V, Watanabe CK, Williams PM, Wood WI;
XX
DR WPI; 2000-412154/35.
DR P-PSDB; AAB24430.
XX
PT Nucleic acids encoding PRO polypeptides useful for preventing, diagnosing
PT and treating diagnosing a cardiovascular, endothelial or angiogenic
PT disorders in mammals.
XX
PS Claim 61; Fig 85; 315pp; English.
XX

The present invention describes nucleic acids encoding PRO polypeptides
useful for preventing, diagnosing and treating diagnosing a
cardiovascular, endothelial or angiogenic disorder in mammals by
modulating cell proliferation, angiogenesis and cardiovascularisation,
and for identifying agonists and antagonists of these processes. The
nucleic acids and the proteins they encode may be used in the prevention,
treatment and diagnosis of diseases associated with inappropriate PRO
expression such as cardiovascular, endothelial or angiogenic disorders in
mammals (e.g. atherosclerosis, cancers and cardiac hypertrophy). For

CC example, the nucleic acids (NCs) and vectors containing them and the PRO
CC polypeptide may be used to treat disorders associated with decreased PRO
CC expression. AAA77510 to AAA77721 and AAB24388 to AAB24435 represent
CC nucleotide and protein sequences used in the exemplification of the
CC present invention
XX
SQ Sequence 1346 BP; 457 A; 245 C; 237 G; 407 T; 0 U; 0 Other;

Query Match 100.0%; Score 1346; DB 3; Length 1346;
Best Local Similarity 100.0%; Pred. No. 1.6e-262;
Matches 1346; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAAGAATGTTGTGGCTGCTCTTTTCTGGTGACTGCCATTTCATGCTGAACCTCTGTCAA 60
Db 1 GAAAGAATGTTGTGGCTGCTCTTTTCTGGTGACTGCCATTTCATGCTGAACCTCTGTCAA 60

QY 61 CCAGGTGCAGAAATGCTTTTAAAGTGAGACTTATCAGAACAGCTCTGGGAGATAAA 120
Db 61 CCAGGTGCAGAAATGCTTTTAAAGTGAGACTTATCAGAACAGCTCTGGGAGATAAA 120

QY 121 GCATATGCTGGGATACCAATGAAGTAATACCTCTTCAAGCGATGCTAGCTTTCTCCATG 180
Db 121 GCATATGCTGGGATACCAATGAAGTAATACCTCTTCAAGCGATGCTAGCTTTCTCCATG 180

QY 181 AGAAAAGTTCCTCCACAGAGAGCAAGCAAGCAAGAAATTTCCCATGTCTTGTCAATGTAAC 240
Db 181 AGAAAAGTTCCTCCACAGAGAGCAAGCAAGCAAGAAATTTCCCATGTCTTGTCAATGTAAC 240

QY 241 CAGAGGGTATCATCTCTGTTTGTGGTTACAGACCCCTTCAAAAATCACACCCCTTCTCTGCT 300
Db 241 CAGAGGGTATCATCTCTGTTTGTGGTTACAGACCCCTTCAAAAATCACACCCCTTCTCTGCT 300

QY 301 GTTGAGGTGCAATCAGCCATAGAATGAACAAGAACCGGATCAACAATGCCCTTCTTTCTA 360
Db 301 GTTGAGGTGCAATCAGCCATAGAATGAACAAGAACCGGATCAACAATGCCCTTCTTTCTA 360

QY 361 AATGACCAACTCTGGAATTTTAAATAATCCCTTCCACACATTTGCACCAACCCATGGACCCA 420
Db 361 AATGACCAACTCTGGAATTTTAAATAATCCCTTCCACACATTTGCACCAACCCATGGACCCA 420

QY 421 TCTGTGCCCATCTGGATTATATATTTTGTGTGATATTTTGCATCATATAGTTGCAATT 480
Db 421 TCTGTGCCCATCTGGATTATATATTTTGTGTGATATTTTGCATCATATAGTTGCAATT 480

QY 481 GCACTACTGATTTTATCAGGATCTGGCAACGTAAGAAGAAAGAAACCAATCTGAA 540
Db 481 GCACTACTGATTTTATCAGGATCTGGCAACGTAAGAAGAAAGAAACCAATCTGAA 540

QY 541 GTGGATGACGCTGAAGATAAGTGTGAAACATGATCACAATTTGAAAATGGCATCCCTCT 600
Db 541 GTGGATGACGCTGAAGATAAGTGTGAAACATGATCACAATTTGAAAATGGCATCCCTCT 600

QY 601 GATCCCCCTGACATGAAGGGGGGCATATTAATGATGCTTTCATGACAGAGGATGAGAGGC 660
Db 601 GATCCCCCTGACATGAAGGGGGGCATATTAATGATGCTTTCATGACAGAGGATGAGAGGC 660

QY 661 TCACCCCTCTCTGAAGGGCTGTGTTCTGCTTCTCAAGAAATTAACATTTGTTCTGT 720
Db 661 TCACCCCTCTCTGAAGGGCTGTGTTCTGCTTCTCAAGAAATTAACATTTGTTCTGT 720

QY 721 GTGACTGCTGAGCATCTGAAATACCAAGAGCAGATCATATATTTGTTTCCACCAATCTT 780
Db 721 GTGACTGCTGAGCATCTGAAATACCAAGAGCAGATCATATATTTGTTTCCACCAATCTT 780

QY 781 CTTTGTATAAATTTTGAATGTGCTTGAAGTGAAGAAAGCAATCAATATATACCCCAAC 840
Db 781 CTTTGTATAAATTTTGAATGTGCTTGAAGTGAAGAAAGCAATCAATATATATACCCCAAC 840

QY 841 ACCACTGAATCATAGCTATTACGACTCAAAATATTCTAAATATTTTCTGACAGTA 900
Db 841 ACCACTGAATCATAGCTATTACGACTCAAAATATTCTAAATATTTTCTGACAGTA 900

QY 901 TAGTGTATAAATGTGGTCACTGTGGTATTGTTGTAGTTATTGATTAAAGCAATTTTAGAATA 960

Db 901 TAGTGATAAATGTTGTCATGTTGTTATTTGTTAGTTTAAAGCATTTTGTAGAAATA 960
Qy 961 AGATCAGGCATATGTATATATTTTTCACACTTCAAGACCTAAGGAAATAAATTTTCCA 1020
Db 961 AGATCAGGCATATGTATATATTTTTCACACTTCAAGACCTAAGGAAATAAATTTTCCA 1020
Qy 1021 GTGGAGATAACATATATATGTTGTTAGAAATCATTTGAAATGGATCCTTTTTCAGCATCA 1080
Db 1021 GTGGAGATAACATATATATGTTGTTAGAAATCATTTGAAATGGATCCTTTTTCAGCATCA 1080
Qy 1081 CTTATATCACTCTGTATATGACTAAGTAAACAAAGTGAGAAATTAATTTGTAATGGA 1140
Db 1081 CTTATATCACTCTGTATATGACTAAGTAAACAAAGTGAGAAATTAATTTGTAATGGA 1140
Qy 1141 TGGATAAATAATGGAATTTACTATATACAGGGTGAATTTTATCCTGTTATCACACCAACA 1200
Db 1141 TGGATAAATAATGGAATTTACTATATACAGGGTGAATTTTATCCTGTTATCACACCAACA 1200
Qy 1201 GTTGATTATATATTTTCTGTAATATCAGCCCTTAATAGGACAATTTCTATTTGTTGACCAAT 1260
Db 1201 GTTGATTATATATTTTCTGTAATATCAGCCCTTAATAGGACAATTTCTATTTGTTGACCAAT 1260
Qy 1261 TCTACAAATTTGTAAAGTCCAACTCTGTGCTAACTTAATAAGTAATAATCATCTCTTTT 1320
Db 1261 TCTACAAATTTGTAAAGTCCAACTCTGTGCTAACTTAATAAGTAATAATCATCTCTTTT 1320
Qy 1321 AAAAAAATAAATAAATAAATAAATAA 1346
Db 1321 AAAAAAATAAATAAATAAATAAATAA 1346

RESULT 4

AAS21484

ID AAS21484 standard; cDNA; 1346 BP.

XX

AC AAS21484;

XX

DT 24-OCT-2001 (first entry)

XX Human cDNA sequence encoding for PRO1312 polypeptide.

DE Human secretory and transmembrane; PRO; mammalian; cancer; lung; breast;

XX prostate; cervical; tumour necrosis factor-alpha; TNF-alpha; cartilage;

KW ear; proliferation; glucose; free fatty acid; skeletal muscle; adipocyte;

KW A-peptide; factor VIIA; gene therapy; ss.

XX Homo sapiens.

OS

XX WO200140466-A2.

PN

XX 07-JUN-2001.

PD

XX 01-DEC-2000; 2000WO-US032678.

PF

XX 01-DEC-1999; 99WO-US028301.

XX 01-DEC-1999; 99WO-US028634.

PR 02-DEC-1999; 99WO-US028551.

PR 02-DEC-1999; 99WO-US028564.

PR 02-DEC-1999; 99WO-US028565.

PR 09-DEC-1999; 99US-0170262P.

PR 16-DEC-1999; 99WO-US030095.

PR 20-DEC-1999; 99WO-US030911.

PR 20-DEC-1999; 99WO-US030999.

PR 30-DEC-1999; 99WO-US031243.

PR 30-DEC-1999; 99WO-US031274.

PR 05-JAN-2000; 2000WO-US000219.

PR 06-JAN-2000; 2000WO-US000277.

PR 06-JAN-2000; 2000WO-US000376.

PR 11-FEB-2000; 2000WO-US003565.

PR 18-FEB-2000; 2000WO-US004341.

PR 18-FEB-2000; 2000WO-US004342.

PR 22-FEB-2000; 2000WO-US004414.

PR 24-FEB-2000; 2000WO-US004914.
PR 24-FEB-2000; 2000WO-US005004.
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005841.
PR 03-MAR-2000; 2000US-0187202P.
PR 10-MAR-2000; 2000WO-US006319.
PR 15-MAR-2000; 2000WO-US006884.
PR 20-MAR-2000; 2000WO-US007377.
PR 21-MAR-2000; 2000WO-US007532.
PR 30-MAR-2000; 2000WO-US008439.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 05-JUN-2000; 2000US-0209832P.
PR 28-JUL-2000; 2000WO-US020710.
PR 11-AUG-2000; 2000WO-US022031.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000WO-US030952.
PR 10-NOV-2000; 2000WO-US030873.

(GETH) GENENTECH INC.

Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;

Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;

Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;

WPI; 2001-408281/43.

P-PSDB; AAU12412.

Isolated , secretory and transmembrane PRO polypeptide used to detect other PRO polypeptides, link bioactive molecules to cells expressing PRO polypeptides, and detect the presence of mammalian tumors e.g. lung, breast, prostate, cervical.

Claim 3; Fig 481; 813pp; English.

AAS21244-AAS21518 encode for novel human secretory and transmembrane PRO polypeptides. The PRO polypeptides are useful to detect other PRO polypeptides, to link bioactive molecules to cells expressing PRO polypeptides, to modulate biological activities of cells expressing PRO polypeptides, and to detect the presence of mammalian lung, colon, breast, prostate, rectal, cervical or liver tumours by comparing PRO polypeptide expression in a cell sample to that in a control sample. Some of the 275 sequences are also useful to stimulate the release of tumour necrosis factor-alpha (TNF-alpha) from human blood, the proliferation or differentiation of chondrocytes, the proliferation or gene expression in pericyte cells, the release of proteoglycans from cartilage, the proliferation of inner ear utricular supporting cells or of T-lymphocytes, the release of a cytokine from peripheral blood monocytes (PBMCs), or the proliferation of endothelial cells. Some of the PRO polypeptides may modulate glucose or free fatty acid uptake by skeletal muscle cells or by adipocytes; or inhibit binding of A-peptide to factor VIIA. The PRO polypeptides can be used in assays to identify molecules involved in binding interactions. The polynucleotides encoding PRO polypeptides can be used to generate probes, antisense RNA/DNA, transgenic or knock out animals and can be used in gene therapy

Sequence 1346 BP; 457 A; 245 C; 237 G; 407 T; 0 U; 0 Other;

Query Match 100.0%; Score 1346; DB 4; Length 1346;

Best Local Similarity 100.0%; Pred. No. 1.6e-262;

Matches 1346; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAAGAAATGTTGGCTGCTCTTTTCTGCTGACTGCCATTTCATGTAACCTGTCAA 60

Db 1 GAAAGAAATGTTGGCTGCTCTTTTCTGCTGACTGCCATTTCATGTAACCTGTCAA 60

Qy 61 CCAGGTGCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAA 120

Db 61 CCAGGTGCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAA 120

QY 121 GCATATGCTGGGATACCAATGAAGAAATACCTCTTCAAGCGATGGTAGCTTTCTCCATG 180
DB 121 GCATATGCTGGGATACCAATGAAGAAATACCTCTTCAAGCGATGGTAGCTTTCTCCATG 180
QY 181 AGAAAAGTTCCCAACAGAGAAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACC 240
DB 181 AGAAAAGTTCCCAACAGAGAAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACC 240
QY 241 CAGAGGGTATCAATCTGGTTTGTGGTTACAGACCTTCAAAAATCAACACCTTCCTGCT 300
DB 241 CAGAGGGTATCAATCTGGTTTGTGGTTACAGACCTTCAAAAATCAACACCTTCCTGCT 300
QY 301 GTTGAGGTGCAATCAGCCATAGAATGAACAAAGAACCGGATCAACAATGCCCTTCTTCTA 360
DB 301 GTTGAGGTGCAATCAGCCATAGAATGAACAAAGAACCGGATCAACAATGCCCTTCTTCTA 360
QY 361 AATGACCAAACTCTGGAATTTTAAAAAATCCCTTCCACACTTGACCCATGGACCCA 420
DB 361 AATGACCAAACTCTGGAATTTTAAAAAATCCCTTCCACACTTGACCCATGGACCCA 420
QY 421 TCTGTGCCCATCTGGATTAATTAATTTGGTGTGATATTTTGCATCATATAGTGCAATT 480
DB 421 TCTGTGCCCATCTGGATTAATTAATTTGGTGTGATATTTTGCATCATATAGTGCAATT 480
QY 481 GCACTACTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACCAAGAACCATCTGAA 540
DB 481 GCACTACTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACCAAGAACCATCTGAA 540
QY 541 GTGATGACGCTGAAGATAAGTGTGAAGAACATGATCACAAATTTGAAATGGCATCCCTCT 600
DB 541 GTGATGACGCTGAAGATAAGTGTGAAGAACATGATCACAAATTTGAAATGGCATCCCTCT 600
QY 601 GATCCCTGGACATGAAGGGGGCATATTAATGATGCTTTCATGACAGAGATGAGAGGC 660
DB 601 GATCCCTGGACATGAAGGGGGCATATTAATGATGCTTTCATGACAGAGATGAGAGGC 660
QY 661 TCACCCCTCTCTGAAGGGCTGTGTTCTGCTTCTCAAGAAATTAACCAATTTGTTCTGT 720
DB 661 TCACCCCTCTCTGAAGGGCTGTGTTCTGCTTCTCAAGAAATTAACCAATTTGTTCTGT 720
QY 721 GTGACTGCTGAGCATCTGAATFACCAAGAGCAGATCATATATTTGTTTCCACATTTCT 780
DB 721 GTGACTGCTGAGCATCTGAATFACCAAGAGCAGATCATATATTTGTTTCCACATTTCT 780
QY 781 CTTTGTATAAATTTTGAATGTCTTGAAAGTGAAAGCAATCAATATATACCCACCAAC 840
DB 781 CTTTGTATAAATTTTGAATGTCTTGAAAGTGAAAGCAATCAATATATACCCACCAAC 840
QY 841 ACCACTGAAATCATAAGCTATTTCAGCATCAAAATATTCTAAATATTTTCTGACAGTA 900
DB 841 ACCACTGAAATCATAAGCTATTTCAGCATCAAAATATTCTAAATATTTTCTGACAGTA 900
QY 901 TAGTGATAAATGTGTCATGCTGATTTTGTAGTATTGATTTAAGCATTTTGTAGAAATA 960
DB 901 TAGTGATAAATGTGTCATGCTGATTTTGTAGTATTGATTTAAGCATTTTGTAGAAATA 960
QY 961 AGATCAGGCATATGTATATATTTTACACTTCAAGACCTAAGCAAAAATAAATTTTCCA 1020
DB 961 AGATCAGGCATATGTATATATTTTACACTTCAAGACCTAAGCAAAAATAAATTTTCCA 1020
QY 1021 GTGAGAAATACATATAATATGTTGTAGAAATCAATGAAATGGATCCTTTTTCACGATCA 1080
DB 1021 GTGAGAAATACATATAATATGTTGTAGAAATCAATGAAATGGATCCTTTTTCACGATCA 1080
QY 1081 CTTATATCACTCTGTATATGACTAAGTAAACAAAAGTGAGAGTAATTTATGTAATGGA 1140
DB 1081 CTTATATCACTCTGTATATGACTAAGTAAACAAAAGTGAGAGTAATTTATGTAATGGA 1140
QY 1141 TGGATAAAAATGGAATTAATCTATATACAGGGTGAATTTTATCTGTTATCACCAACA 1200
DB 1141 TGGATAAAAATGGAATTAATCTATATACAGGGTGAATTTTATCTGTTATCACCAACA 1200
QY 1201 GTTGATTATATATTTTCTGAATATCAGCCCTTAATAGGACAATTTCTATTTGTGACCAAT 1260

DB 1201 GTTGATTATATATTTTCTGAATATCAGCCCTTAATAGGACAATTTCTATTTGTGACCAAT 1260
QY 1261 TCTACAATTTGTAAAAAGTCCCAATCTGTGCTAATCTTAATAAGTAATAATCATCTCTTTT 1320
DB 1261 TCTACAATTTGTAAAAAGTCCCAATCTGTGCTAATCTTAATAAGTAATAATCATCTCTTTT 1320
QY 1321 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1346
DB 1321 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1346
RESULT 5
AAF44243
ID AAF44243 standard; cDNA; 1346 BP.
XX
AC AAF44243;
XX
DT 02-APR-2001 (first entry)
XX Human PRO1312 (UNQ678) nucleotide sequence SEQ ID NO:386.
DE Human; secreted and transmembrane protein; PRO; cytostatic; cell death;
XX cancer; chromosomal mapping; gene mapping; tissue typing;
KW diagnostic assay; ss.
KW
OS Homo sapiens.
XX
FN WO200073454-A1.
XX
PD 07-DEC-2000.
XX
PP 30-MAR-2000; 2000WO-US008439.
XX
PR 02-JUN-1999; 99WO-US012252.
PR 23-JUN-1999; 99US-0141037P.
PR 07-JUL-1999; 99US-0143048P.
PR 20-JUL-1999; 99US-0144758P.
PR 26-JUL-1999; 99US-0145698P.
PR 28-JUL-1999; 99US-0146222P.
PR 17-AUG-1999; 99US-0149396P.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 08-OCT-1999; 99US-0158663P.
PR 30-NOV-1999; 99WO-US028313.
PR 01-DEC-1999; 99WO-US028301.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US004914.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 15-MAR-2000; 2000WO-US006884.
PR 20-MAR-2000; 2000WO-US007377.
XX
(GETH) GENENTECH INC.
XX Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
PI Ferrara N, Fong S, Gerber H, Gerritsen MB, Goddard A, Godowski PJ;
PI Grimaldi CJ, Gurney AL, Kljavin IJ, Napier MA, Pan J, Paoni NF;
PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;
PI Zhang Z;
XX
DR WP1; 2001-032160/04.
DR P-PSDB; AAB65274.
XX
PT PRO polynucleotides used to produce polypeptides used to target bioactive
PT molecules such as toxins, radiolabels or antibodies, to specific cells,
PT to cause targeted cell death.

XX Claim 2; Fig 277; 935pp; English.

XX The present invention describes human secreted and transmembrane PRO proteins. The PRO proteins have cytosolic activity. The PRO proteins can be used for targeted delivery of bioactive molecules, such as toxins, radiolabels or antibodies, that cause cell death. PRO nucleotide sequences, and their fragments, can be used as hybridisation probes, in chromosomal and gene mapping, and in the generation of anti-sense RNA and DNA. They may also be used to produce transgenic animals which are used to develop and screen therapeutically useful reagents. The PRO nucleotide and protein sequence can be used for tissue typing and in treating cancer. Anti-PRO antibodies can be used in diagnostic assays. AAF44270 to AAF44470 represent PCR primers and hybridisation probes used in the isolation of human PRO sequences. AAF44087 to AAF44269 and AAB55154 to AAB5300 represent human PRO polynucleotide and protein sequences given in the exemplification of the present invention

SQ Sequence 1346 BP; 457 A; 245 C; 237 G; 407 T; 0 U; 0 Other;

Query Match 100.0%; Score 1346; DB 5; Length 1346;

Best Local Similarity 100.0%; Pred. No. 1.6e-262;

Matches 1346; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAAGATGTTGGCTGCTCTTTTCTGGTGACTGCCATTGCTGAACTCTGCAA 60

DB 1 GAAAGATGTTGGCTGCTCTTTTCTGGTGACTGCCATTGCTGAACTCTGCAA 60

QY 61 CCAGGTGCAGAAATGCTTTTAAAGTGAGACTTAGTATCAGACAGCTCTGGGAGATAA 120

DB 61 CCAGGTGCAGAAATGCTTTTAAAGTGAGACTTAGTATCAGACAGCTCTGGGAGATAA 120

QY 121 GCATATGCTGGGATACCAATGAAGATACCTCTTCAAGCGATGGTAGCTTCTCCATG 180

DB 121 GCATATGCTGGGATACCAATGAAGATACCTCTTCAAGCGATGGTAGCTTCTCCATG 180

QY 181 AGAAAGTTCCTCCACAGAGAGCAACAGAAATTTCCCATGCTCCTACTTGGCAATGTAAC 240

DB 181 AGAAAGTTCCTCCACAGAGAGCAACAGAAATTTCCCATGCTCCTACTTGGCAATGTAAC 240

QY 241 CAGAGGTATCATTTCTGGTTTGTGGTTTACAGACCCCTTCAAAAATCAGACCCCTTCTGCT 300

DB 241 CAGAGGTATCATTTCTGGTTTGTGGTTTACAGACCCCTTCAAAAATCAGACCCCTTCTGCT 300

QY 301 GTTGAGTGCATATCAGCCATAGAAATGAACAAGAACCGGATCAACATGCTTCTTCTA 360

DB 301 GTTGAGTGCATATCAGCCATAGAAATGAACAAGAACCGGATCAACATGCTTCTTCTA 360

QY 361 AATGACCAAACTCTGGAATTTTAAATCCCTTCCACACTTGCACACCCATGGACCCA 420

DB 361 AATGACCAAACTCTGGAATTTTAAATCCCTTCCACACTTGCACACCCATGGACCCA 420

QY 421 TCTGTGCCATCTGGATATATATTTGGTGTGATATTTGGATCATCATAGTTGCAAT 480

DB 421 TCTGTGCCATCTGGATATATATTTGGTGTGATATTTGGATCATCATAGTTGCAAT 480

QY 481 GCATCTGATTTTATCAGGGATCTGGCAACGTAGAGAAAGAAACAAGAACCATCTGAA 540

DB 481 GCATCTGATTTTATCAGGGATCTGGCAACGTAGAGAAAGAAACAAGAACCATCTGAA 540

QY 541 GTGGATGACGCTGAAGATTAAGTGTGAATAACATGATCAATTTGAAATGGCATCCCCTCT 600

DB 541 GTGGATGACGCTGAAGATTAAGTGTGAATAACATGATCAATTTGAAATGGCATCCCCTCT 600

QY 601 GATCCCCTGGACATGAAGGGGGCATATTAATGATGCTTTCATGACAGAGGATGAGGC 660

DB 601 GATCCCCTGGACATGAAGGGGGCATATTAATGATGCTTTCATGACAGAGGATGAGGC 660

QY 661 TCACCCCTCTCTGAAGGGCTGTTGTTCTGCTTCTCCTCAAGAAATTAACAATTTGTTCTGT 720

DB 661 TCACCCCTCTCTGAAGGGCTGTTGTTCTGCTTCTCCTCAAGAAATTAACAATTTGTTCTGT 720

QY 721 GTGACTGCTGAGCATCCTGAAATACCAAGAGCAGATCATATATTTTGTTCACCATTTCTT 780

DB 721 GTGACTGCTGAGCATCCTGAAATACCAAGAGCAGATCATATATTTTGTTCACCATTTCTT 780

QY 781 CTTTGTAAATAAATTTTGAATGCTGCTGAAAGTGAAAGCAATCAATATATACCCACCAAC 840

DB 781 CTTTGTAAATAAATTTTGAATGCTGCTGAAAGTGAAAGCAATCAATATATACCCACCAAC 840

QY 841 ACCACTGAAATCATAAGCTATTTCAGACTCAAAATATTCTAAATATTCTTGACAGTA 900

DB 841 ACCACTGAAATCATAAGCTATTTCAGACTCAAAATATTCTAAATATTCTTGACAGTA 900

QY 901 TAGTGATAAATGCTGCTCATGCTGATTTTGTAGTTATTGATTAAAGCAATTTTAGAATA 960

DB 901 TAGTGATAAATGCTGCTCATGCTGATTTTGTAGTTATTGATTAAAGCAATTTTAGAATA 960

QY 961 AGATCAGGCATATGTATATATTTTACACACTTCAAGACCTTAAGGAAAAATAAATTTTCCA 1020

DB 961 AGATCAGGCATATGTATATATTTTACACACTTCAAGACCTTAAGGAAAAATAAATTTTCCA 1020

QY 1021 GTGGAGATACATATAATATGCTGTAGAAATCATTTGAAATGGATCCTTTTGTGACGATCA 1080

DB 1021 GTGGAGATACATATAATATGCTGTAGAAATCATTTGAAATGGATCCTTTTGTGACGATCA 1080

QY 1081 CTTATATCACTCTGTATATGACTAAGTAAACAAAGTGAGAAATTAATTATTGTAATGGA 1140

DB 1081 CTTATATCACTCTGTATATGACTAAGTAAACAAAGTGAGAAATTAATTATTGTAATGGA 1140

QY 1141 TGGATAAATAATGGAATTAATCATATACAGGGTGGAAATTTTATCCTGTTATCACACCAACA 1200

DB 1141 TGGATAAATAATGGAATTAATCATATACAGGGTGGAAATTTTATCCTGTTATCACACCAACA 1200

QY 1201 GTTGATATATATTTTCTGAATATCAGCCCTTAATAGGACAAATTTCTATTGTTGACCAAT 1260

DB 1201 GTTGATATATATTTTCTGAATATCAGCCCTTAATAGGACAAATTTCTATTGTTGACCAAT 1260

QY 1261 TCTACAATTTGTAAGTCCAAATCTGTGCTAACTTAAAGTAATAATATCATCTCTTTT 1320

DB 1261 TCTACAATTTGTAAGTCCAAATCTGTGCTAACTTAAAGTAATAATATCATCTCTTTT 1320

QY 1321 AAAAAAAAAAAAAAAAAAAAAAAAAA 1346

DB 1321 AAAAAAAAAAAAAAAAAAAAAAAAAA 1346

RESULT 6

ABX77959

ID ABX77959 standard; cDNA; 1346 BP.

XX

AC ABX77959;

XX

DT 14-APR-2003 (first entry)

XX

DE Human PRO polynucleotide #121.

XX

KW Human; PRO; gene; ss; cytostatic; tumour; cancer; breast; lung; stomach; liver; horse; cow; dog; cat; sheep; pig; goat; rabbit; ADEPT;

KW antibody-dependent enzyme mediated prodrug therapy.

XX

OS Homo sapiens.

XX

PN US2003027163-A1.

XX

PD 06-FEB-2003.

XX

PF 15-NOV-2001; 2001US-00997666.

XX

PR 16-JUN-1997; 97US-0049787P.

PR 17-OCT-1997; 97US-0062250P.

PR 05-NOV-1997; 97WO-US020069.

PR 12-NOV-1997; 97US-0065186P.

PR 13-NOV-1997; 97US-0065311P.

PR 24-NOV-1997; 97US-0066770P.

PR 25-FEB-1998; 98US-0075945P.

PR 20-MAR-1998; 98US-0078910P.
PR 28-APR-1998; 98US-0083322P.
PR 07-MAY-1998; 98US-0084600P.
PR 28-MAY-1998; 98US-0087106P.
PR 02-JUN-1998; 98US-0087607P.
PR 02-JUN-1998; 98US-0087609P.
PR 02-JUN-1998; 98US-0087759P.
PR 03-JUN-1998; 98US-0087827P.
PR 04-JUN-1998; 98US-0088021P.
PR 04-JUN-1998; 98US-0088025P.
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PR 10-JUN-1998; 98US-0088810P.
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PR 10-JUN-1998; 98US-0088826P.
PR 11-JUN-1998; 98US-0088858P.
PR 11-JUN-1998; 98US-0088861P.
PR 11-JUN-1998; 98US-0088876P.
PR 12-JUN-1998; 98US-0089105P.
PR 16-JUN-1998; 98US-0089440P.
PR 16-JUN-1998; 98US-0089512P.
PR 16-JUN-1998; 98US-0089514P.
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PR 17-JUN-1998; 98US-0089600P.
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PR 18-JUN-1998; 98US-0089907P.
PR 18-JUN-1998; 98US-0089908P.
PR 19-JUN-1998; 98US-0089947P.
PR 19-JUN-1998; 98US-0089948P.
PR 19-JUN-1998; 98US-0089952P.
PR 22-JUN-1998; 98US-0090246P.
PR 22-JUN-1998; 98US-0090252P.
PR 22-JUN-1998; 98US-0090254P.
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PR 24-JUN-1998; 98US-0090472P.
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PR 24-JUN-1998; 98US-0090542P.
PR 24-JUN-1998; 98US-0090557P.
PR 25-JUN-1998; 98US-0090676P.
PR 25-JUN-1998; 98US-0090678P.
PR 25-JUN-1998; 98US-0090690P.
PR 25-JUN-1998; 98US-0090694P.
PR 25-JUN-1998; 98US-0090695P.
PR 25-JUN-1998; 98US-0090696P.
PR 26-JUN-1998; 98US-0090862P.
PR 26-JUN-1998; 98US-0090863P.
PR 01-JUL-1998; 98US-0091360P.
PR 01-JUL-1998; 98US-0091544P.
PR 02-JUL-1998; 98US-0091478P.
PR 02-JUL-1998; 98US-0091519P.

PR 02-JUL-1998; 98US-0091626P.
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PR 02-JUL-1998; 98US-0091633P.
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PR 07-JUL-1998; 98US-0091978P.
PR 07-JUL-1998; 98US-0091982P.
PR 09-JUL-1998; 98US-0092182P.
PR 10-JUL-1998; 98US-0092472P.
PR 20-JUL-1998; 98US-0093339P.
PR 30-JUL-1998; 98US-0094651P.
PR 04-AUG-1998; 98US-0095282P.
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PR 04-AUG-1998; 98US-0095301P.
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PR 11-AUG-1998; 98US-0096146P.
PR 12-AUG-1998; 98US-0096329P.
PR 17-AUG-1998; 98US-0096757P.
PR 17-AUG-1998; 98US-0096766P.
PR 17-AUG-1998; 98US-0096768P.
PR 17-AUG-1998; 98US-0096773P.
PR 17-AUG-1998; 98US-0096791P.
PR 17-AUG-1998; 98US-0096867P.
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PR 17-AUG-1998; 98US-0096894P.
PR 17-AUG-1998; 98US-0096895P.
PR 17-AUG-1998; 98US-0096897P.
PR 18-AUG-1998; 98US-0096949P.
PR 18-AUG-1998; 98US-0096950P.
PR 18-AUG-1998; 98US-0096959P.
PR 18-AUG-1998; 98US-0096960P.
PR 18-AUG-1998; 98US-0097022P.
PR 19-AUG-1998; 98US-0097141P.
PR 20-AUG-1998; 98US-0097218P.
PR 24-AUG-1998; 98US-0097661P.
PR 26-AUG-1998; 98US-0097952P.
PR 26-AUG-1998; 98US-0097955P.
PR 26-AUG-1998; 98US-0097971P.
PR 26-AUG-1998; 98US-0097974P.
PR 26-AUG-1998; 98US-0097978P.
PR 26-AUG-1998; 98US-0097979P.
PR 26-AUG-1998; 98US-0097986P.
PR 26-AUG-1998; 98US-0098014P.
PR 31-AUG-1998; 98US-0098525P.
PR 16-SEP-1998; 98US-0100634P.
PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98US-0100858P.
PR 17-SEP-1998; 98WO-US019437.
PR 07-OCT-1998; 98WO-US021141.
PR 01-DEC-1998; 98WO-US025108.
PR 22-DEC-1998; 98US-0113296P.
PR 05-JAN-1999; 99WO-US000106.
PR 08-MAR-1999; 99WO-US005028.
PR 12-MAR-1999; 99US-0123957P.
PR 02-JUN-1999; 99WO-US012252.
PR 23-JUN-1999; 99US-0141037P.
PR 07-JUL-1999; 99US-0143048P.
PR 20-JUL-1999; 99US-0144758P.
PR 26-JUL-1999; 99US-0145698P.
PR 28-JUL-1999; 99US-0146222P.
PR 17-AUG-1999; 99US-0149396P.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 08-OCT-1999; 99US-0158663P.
PR 30-NOV-1999; 99WO-US028313.

PR	01-DEC-1999;	99WO-US028301.	
PR	01-DEC-1999;	99WO-US028634.	
PR	16-DEC-1999;	99WO-US030095.	
PR	20-DEC-1999;	99WO-US030911.	
PR	05-JAN-2000;	2000WO-US000219.	
PR	06-JAN-2000;	2000WO-US000376.	
PR	11-FEB-2000;	2000WO-US0003565.	
PR	18-FEB-2000;	2000WO-US004341.	
PR	22-FEB-2000;	2000WO-US004414.	
PR	24-FEB-2000;	2000WO-US004914.	
PR	24-FEB-2000;	2000WO-US005004.	
PR	02-MAR-2000;	2000WO-US005841.	
PR	10-MAR-2000;	2000WO-US006319.	
PR	15-MAR-2000;	2000WO-US006884.	
PR	20-MAR-2000;	2000WO-US007377.	
PR	30-MAR-2000;	2000WO-US008439.	
PR	15-MAY-2000;	2000WO-US013358.	
PR	17-MAY-2000;	2000WO-US013705.	
PR	22-MAY-2000;	2000WO-US014042.	
PR	30-MAY-2000;	2000WO-US014941.	
PR	02-JUN-2000;	2000WO-US015264.	
PR	23-JUN-2000;	2000US-0213637P.	
PR	28-JUL-2000;	2000WO-US020710.	
PR	11-AUG-2000;	2000WO-US022031.	
PR	23-AUG-2000;	2000WO-US023522.	
PR	24-AUG-2000;	2000WO-US023328.	
PR	07-SEP-2000;	2000US-0230978P.	
Query Match 100.0%; Score 1346; DB 7; Length 1346;			
Best Local Similarity 100.0%; Pred. No. 1.6e-262;			
Matches 1346; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
QY	1	GAAGAATGTTGGGCTGCTCTTTTCTGGTGACTGCCATTCTGCTGAACTCTGTCAA	60
Db	1	GAAGAATGTTGGGCTGCTCTTTTCTGGTGACTGCCATTCTGCTGAACTCTGTCAA	60
QY	61	CCAGGTGCAGAAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAA	120
Db	61	CCAGGTGCAGAAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAA	120
QY	121	GCATATGCTGGGATACCAATGAAGAAATACCTCTTCAAAGCGATGGTAGCTTCTCCATG	180
Db	121	GCATATGCTGGGATACCAATGAAGAAATACCTCTTCAAAGCGATGGTAGCTTCTCCATG	180
QY	181	AGAAAGTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCTTACATTTGCAATGTAACC	240
Db	181	AGAAAGTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCTTACATTTGCAATGTAACC	240
QY	241	CAGAGGTATCATTTCTGGTTTGTGGTTACAGACCTTCAAAAAATCACACCTTCTCTGCT	300
Db	241	CAGAGGTATCATTTCTGGTTTGTGGTTACAGACCTTCAAAAAATCACACCTTCTCTGCT	300
QY	301	GTTGAGTGCATATCAGCCATAAAGAAATGAACAAGACCGGATCAACAATGCTTCTTTCTA	360
Db	301	GTTGAGTGCATATCAGCCATAAAGAAATGAACAAGACCGGATCAACAATGCTTCTTTCTA	360
QY	361	AATGACCAAACTCTGGAAATTTTAAAAATCCCTTCCACACTTGCACCCATGGACCCA	420
Db	361	AATGACCAAACTCTGGAAATTTTAAAAATCCCTTCCACACTTGCACCCATGGACCCA	420
QY	421	TCTGTGCCCATCTGGATTATATATTGGTGTGATATTGTCATCATCATAGTTGCAATT	480
Db	421	TCTGTGCCCATCTGGATTATATATTGGTGTGATATTGTCATCATCATAGTTGCAATT	480
QY	481	GCACTACTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAA	540
Db	481	GCACTACTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAA	540
QY	541	GTGGATGACCTGAAGATAAGTGTGAAACATGATCACAAATTTGAAATGGCATCCCTCT	600
Db	541	GTGGATGACCTGAAGATAAGTGTGAAACATGATCACAAATTTGAAATGGCATCCCTCT	600
QY	601	GATCCCCCTGGACATGAAGGGGGGCATATTAAATGATGCCCTTCATGACAGAGGATGAGAGC	660

Db	601	GATCCCCCTGGACATGAAGGGGGGCATATTAAATGATGCCCTTCATGACAGAGGATGAGAGC	660
QY	661	TCACCCCTCTCTGAAGGCTGTTGTTCTGCTTCTCAAGAAATTAACATTTGTTCTGT	720
Db	661	TCACCCCTCTCTGAAGGCTGTTGTTCTGCTTCTCAAGAAATTAACATTTGTTCTGT	720
QY	721	GTGACTGCTGAGCATCCTGAAATACCAAGAGCAGATCATATATTTTGTTCACCATTTCTT	780
Db	721	GTGACTGCTGAGCATCCTGAAATACCAAGAGCAGATCATATATTTTGTTCACCATTTCTT	780
QY	781	CTTTTGTAAATAAATTTTCAATGTGCTTGAAGTGAAAAGCAATCAATTATACCCACCAAC	840
Db	781	CTTTTGTAAATAAATTTTCAATGTGCTTGAAGTGAAAAGCAATCAATTATACCCACCAAC	840
QY	841	ACCACGTGAAATCATAGCTATTTCAGGCTCAAAATATTCTAAAAATATTTTCTTGACAGTA	900
Db	841	ACCACGTGAAATCATAGCTATTTCAGGCTCAAAATATTCTAAAAATATTTTCTTGACAGTA	900
QY	901	TAGTGATATAAATGTGGTCATGTGGTATTGTAGTTATTGATTTAAGCATTTTGTAGAAATA	960
Db	901	TAGTGATATAAATGTGGTCATGTGGTATTGTAGTTATTGATTTAAGCATTTTGTAGAAATA	960
QY	961	AGATCAGGCATATGTATATATTTTTCACACTTCAAGAGCCCTAAGGAAAAATAAATTTTCCA	1020
Db	961	AGATCAGGCATATGTATATATTTTTCACACTTCAAGAGCCCTAAGGAAAAATAAATTTTCCA	1020
QY	1021	GTGGAGATACATATATATATGGTGTAGAAATCATTTGAAATGGATCCTTTTGACGATCA	1080
Db	1021	GTGGAGATACATATATATATGGTGTAGAAATCATTTGAAATGGATCCTTTTGACGATCA	1080
QY	1081	CTTATATCACTCTGTATATGACTAAGTAAACAAAGTGAGAGTAATTTATTTGTAATGGA	1140
Db	1081	CTTATATCACTCTGTATATGACTAAGTAAACAAAGTGAGAGTAATTTATTTGTAATGGA	1140
QY	1141	TGGATAAAAAATGGAATTTACTCATATACAGGGTGGAAATTTTATCCTGTTATCACCAACA	1200
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QY	1261	TCTACAATTTGTAAAGTCCCAATCTGTGCTAACTTAATAAGTAATAATCATCTCTTTT	1320
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ID	ABX80371	standard; DNA; 1346 BP.	
XX	XX		
AC	ABX80371;		
XX	XX		
DT	28-APR-2003	(first entry)	
XX	XX		
DE	Novel human secreted or transmembrane protein PRO1192 DNA.		
XX	XX		
KW	Human; PRO; hypertrophy of neonatal heart; angiogenesis; wound healing;		
KW	cardiac insufficiency disorder; cancer; tumour; immune response;		
KW	adrenal cortical capillary endothelial growth; c-fos induction;		
KW	vascular endothelial growth factor inhibition; VEGF inhibition;		
KW	endothelial cell growth inhibitor; T-lymphocytes stimulation;		
KW	retinal neurons cell survival; rod photoreceptor cell survival;		
KW	retinal disorder; retinitis pigmentosa; kidney disorder;		
KW	mammalian kidney mesangial cell proliferation; Berger disease;		
KW	dermatitis; herpeticiformis; Crohn's disease; chondrocyte proliferation;		
XX	chondrocyte redifferentiation; sports injury; arthritis; gene; ds.		

OS Homo sapiens.
XX US2002132252-A1.
PN
XX
PD 19-SEP-2002.
XX
PF 14-NOV-2001; 2001US-00990442.
XX
PR 16-JUN-1997; 97US-0049787P.
PR 17-OCT-1997; 97US-0062250P.
PR 05-NOV-1997; 97WO-US020069.
PR 12-NOV-1997; 97US-0065186P.
PR 13-NOV-1997; 97US-0065311P.
PR 24-NOV-1997; 97US-0066770P.
PR 25-FEB-1998; 98US-0075945P.
PR 20-MAR-1998; 98US-0078910P.
PR 28-APR-1998; 98US-0083322P.
PR 07-MAY-1998; 98US-0084600P.
PR 28-MAY-1998; 98US-0087106P.
PR 02-JUN-1998; 98US-0087607P.
PR 02-JUN-1998; 98US-0087609P.
PR 02-JUN-1998; 98US-0087759P.
PR 03-JUN-1998; 98US-0087827P.
PR 04-JUN-1998; 98US-0088021P.
PR 04-JUN-1998; 98US-0088025P.
PR 04-JUN-1998; 98US-0088026P.
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PR 05-JUN-1998; 98US-0088167P.
PR 05-JUN-1998; 98US-0088202P.
PR 05-JUN-1998; 98US-0088212P.
PR 05-JUN-1998; 98US-0088217P.
PR 09-JUN-1998; 98US-0088655P.
PR 10-JUN-1998; 98US-0088734P.
PR 10-JUN-1998; 98US-0088738P.
PR 10-JUN-1998; 98US-0088742P.
PR 10-JUN-1998; 98US-0088810P.
PR 10-JUN-1998; 98US-0088824P.
PR 10-JUN-1998; 98US-0088826P.
PR 11-JUN-1998; 98US-0088858P.
PR 11-JUN-1998; 98US-0088861P.
PR 11-JUN-1998; 98US-0088876P.
PR 12-JUN-1998; 98US-0089105P.
PR 16-JUN-1998; 98US-0089440P.
PR 16-JUN-1998; 98US-0089512P.
PR 16-JUN-1998; 98US-0089514P.
PR 17-JUN-1998; 98US-0089532P.
PR 17-JUN-1998; 98US-0089538P.
PR 17-JUN-1998; 98US-0089598P.
PR 17-JUN-1998; 98US-0089599P.
PR 17-JUN-1998; 98US-0089600P.
PR 17-JUN-1998; 98US-0089653P.
PR 18-JUN-1998; 98US-0089801P.
PR 18-JUN-1998; 98US-0089907P.
PR 18-JUN-1998; 98US-0089908P.
PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98WO-US019437.
PR 07-OCT-1998; 98WO-US021141.
PR 01-DEC-1998; 98WO-US025108.
PR 05-JAN-1999; 99WO-US000106.
PR 08-MAR-1999; 99WO-US005028.
PR 02-JUN-1999; 99WO-US012252.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 30-NOV-1999; 99WO-US028313.
PR 01-DEC-1999; 99WO-US028301.
PR 01-DEC-1999; 99WO-US028634.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 06-JAN-2000; 2000WO-US000219.

PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US004914.
PR 02-MAR-2000; 2000WO-US005004.
PR 10-MAR-2000; 2000WO-US005841.
PR 15-MAR-2000; 2000WO-US006319.
PR 20-MAR-2000; 2000WO-US006884.
PR 30-MAR-2000; 2000WO-US007377.
PR 15-MAY-2000; 2000WO-US013358.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 11-AUG-2000; 2000WO-US022031.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000WO-US030952.
PR 01-DEC-2000; 2000WO-US032678.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-JUN-2001; 2001WO-US017800.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 28-AUG-2001; 2001US-00941992.

(GETH) GENENTECH INC.

Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Baton DL;
Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ;
Grimaldi JC, Gurney AL, Kljavin IJ, Napier MA, Pan J, Paoni NF;
Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;
Zhang Z;

WPI; 2003-247083/24.

P-PSDB; ABUS9168.

Novel isolated PRO polypeptides e.g., PRO826, PRO1068, PRO1184, PRO1346 and PRO1375, which stimulate proliferation of stimulated T-lymphocytes are therapeutically useful for enhancing immune response and in cancer treatments.

Claim 2; Fig 279; 648pp; English.

The invention describes an isolated human PRO polypeptide. The PRO polypeptides are useful in detecting PRO polypeptides in a sample, in linking a bioactive molecule to a cell expressing a PRO polypeptide, and in modulating at least one biological activity of a cell expressing a PRO polypeptide. PRO1312 stimulates hypertrophy of neonatal heart and is thus useful for treating cardiac insufficiency disorders. PRO1154 and PRO1186 stimulate adrenal cortical capillary endothelial growth, and PRO536, PRO943, PRO828, PRO1068 or PRO535, PRO826, PRO819, PRO1126, PRO1360 and PRO1387 induce c-fos in endothelial cells, and are thus useful for treating conditions or disorders where angiogenesis would be beneficial, e.g. wound healing and antagonist of this polypeptide are useful for treating cancerous tumours. PRO812 inhibits vascular endothelial growth factor (VEGF) stimulated proliferation of endothelial cells and is thus useful for inhibiting endothelial cell growth in mammals which would be beneficial in inhibiting tumour growth. PRO826, PRO1068, PRO1184, PRO1346 and PRO1375 stimulate proliferation of stimulated T-lymphocytes and are therapeutically useful for enhancing immune response. PRO828, PRO826, PRO1068 or PRO1132 enhance survival of retinal neurons cells (PRO1132 is also enhances survival/proliferation of rod photoreceptor cells) and therefore are useful for treating retinal disorders of injuries, e.g. retinitis pigmentosa, AMD. PRO819, PRO813 and PRO1066 induce proliferation of mammalian kidney mesangial cells, and therefore are useful for treating kidney disorders associated with decreased mesangial cell function such as Berger disease or other nephropathies associated with dermatitis, herpeticiformis or Crohn's disease. PRO1310, PRO844, PRO1312, PRO1192 and PRO1387 induce the

CC proliferation and/or redifferentiation of chondrocytes in culture and are
CC thus useful for treating sports injuries, and arthritis. This sequence
CC represents a novel human PRO protein polynucleotide

XX
SQ Sequence 1346 BP; 457 A; 245 C; 237 G; 407 T; 0 U; 0 Other;
Query Match 100.0%; Score 1346; DB 7; Length 1346;
Best Local Similarity 100.0%; Pred. No. 1.6e-262;
Matches 1346; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAAGATGTTGGCTGCTCTTTTCTGGTGACTGCAATTCATGCTGAACTCTGTCAA 60
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Qy 61 CCAGGTGAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAA 120
Db |||||||
Qy 61 CCAGGTGAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAA 120
Db |||||||
Qy 121 GCATATGCTGGGATACCAATGAAGATPACCTCTTCAAAGCGATGGTAGCTTCTCCATG 180
Db |||||||
Qy 121 GCATATGCTGGGATACCAATGAAGATPACCTCTTCAAAGCGATGGTAGCTTCTCCATG 180
Db |||||||
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Qy 181 AGAAAGTCCCAACAGAGAACGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAAAC 240
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Qy 241 CAGAGGTATCAITCTGGTTTGTGGTTTACAGACCCCTTCAAANAATCAGACCCCTTCTGCT 300
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Qy 241 CAGAGGTATCAITCTGGTTTGTGGTTTACAGACCCCTTCAAANAATCAGACCCCTTCTGCT 300
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Db |||||||
Qy 301 GTTGAGTGCAATCAGCCATAAGAAATGAACAGAACCGGATCAACAAATGCTTCTTCTA 360
Db |||||||
Qy 361 AATGACCAAACTCTGGAATTTTAAATCCCTTCCACACTTGCACACCCATGGACCCA 420
Db |||||||
Qy 361 AATGACCAAACTCTGGAATTTTAAATCCCTTCCACACTTGCACACCCATGGACCCA 420
Db |||||||
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Db |||||||
Qy 421 TCTGTGCCCATCTGGATTTATATTTGGTGATATTTTGGCATCATCATAGTTGCAATT 480
Db |||||||
Qy 481 GCACACTGATTTTATCAGGGATCTGGCAACGTTAGAGAAAGCAACAAAGAACCATCTGAA 540
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Qy 481 GCACACTGATTTTATCAGGGATCTGGCAACGTTAGAGAAAGCAACAAAGAACCATCTGAA 540
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Qy 601 GATCCCTGGACATGAAGGGGGGCATATTAATGATGCTTTCATGACAGAGGATGAGAGC 660
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Qy 661 TCACCCCTCTCTGAAGGCTGTTGTTCTGCTTCTCAAGAAATTAACATTTGTTTCTGT 720
Db |||||||
Qy 661 TCACCCCTCTCTGAAGGCTGTTGTTCTGCTTCTCAAGAAATTAACATTTGTTTCTGT 720
Db |||||||
Qy 721 GTGACTGCTGAGCATCTGAAATACCAAGAGCAGATCATATATTTTGTTCACCATTCIT 780
Db |||||||
Qy 721 GTGACTGCTGAGCATCTGAAATACCAAGAGCAGATCATATATTTTGTTCACCATTCIT 780
Db |||||||
Qy 781 CTTTGTGTAATAATTTTGAATGTGCTTGAAGTGAAGCAATCAATATATACCCACCAAC 840
Db |||||||
Qy 781 CTTTGTGTAATAATTTTGAATGTGCTTGAAGTGAAGCAATCAATATATACCCACCAAC 840
Db |||||||
Qy 841 ACCACTGAAATCATAGCTATTCCAGCTCAAAATATTTCTAAATATTTTCTGACAGTA 900
Db |||||||
Qy 841 ACCACTGAAATCATAGCTATTCCAGCTCAAAATATTTCTAAATATTTTCTGACAGTA 900
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Qy 901 TAGTGATAAATGTGGTCATGTGGTATTTGTAGTTTATGATTTTAAAGCAATTTTAAATA 960
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Qy 961 AGATCAGGCATATGTATATATTTTTCACACTTCAAAGACCTTAAGGAAAAATAAATTTTCCA 1020
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Db |||||||
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Qy 1081 CTTATATCACTCTGTATATGACTAAGTAAACAAAGTGAAGTAATTAATTTGTAATGGA 1140
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Qy 1141 TGGATAAAAAATGGAATTTACTCATATACAGGGTGAATTTTATCTGTTATCACCACCAACA 1200
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Qy 1141 TGGATAAAAAATGGAATTTACTCATATACAGGGTGAATTTTATCTGTTATCACCACCAACA 1200
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Qy 1201 GTTGATTATATATTTTCTGAATATCAGCCCCCTAATAGGACAAATTTCTATTTGTTGACCAAT 1260
Db |||||||
Qy 1201 GTTGATTATATATTTTCTGAATATCAGCCCCCTAATAGGACAAATTTCTATTTGTTGACCAAT 1260
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Qy 1261 TCTACAATTTGTAAAGTCCCAATCTGTCTAACTTAATAAAGTAATAATCATCTCTTTT 1320
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Qy 1261 TCTACAATTTGTAAAGTCCCAATCTGTCTAACTTAATAAAGTAATAATCATCTCTTTT 1320
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Qy 1321 AAAAAAATAAAAAAATAAAAAA 1346
Db |||||||
Qy 1321 AAAAAAATAAAAAAATAAAAAA 1346
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RESULT 8
ACA69277

ID ACA69277 standard; cDNA; 1346 BP.

XX ACA69277;

XX 26-JUN-2003 (first entry)

XX Human cDNA encoding secreted/transmembrane protein PRO1312.

XX Human; ss; gene; PRO; secreted protein; transmembrane protein;
KW cardiac insufficiency disorders; angiogenesis; wound healing;
KW cancerous tumour; immune response; retinal disorder; sight loss;
KW retinitis pigmentosa; age-related macular degeneration; AMD;
KW kidney disorder; Berger disease; nephropathy; dermatitis; herpeticiformis;
KW Crohn's disease; sports injury; arthritis.

XX Homo sapiens.

XX US2003032023-A1.

XX 13-FEB-2003.

XX 14-NOV-2001; 2001US-00990711.

XX 16-JUN-1997; 97US-0049787P.

XX 17-OCT-1997; 97US-0062250P.

XX 05-NOV-1997; 97WO-US020069.

XX 12-NOV-1997; 97US-0065186P.

XX 13-NOV-1997; 97US-0065311P.

XX 24-NOV-1997; 97US-0066770P.

XX 25-FEB-1998; 98US-0075945P.

XX 20-MAR-1998; 98US-0078910P.

XX 28-APR-1998; 98US-0083322P.

XX 07-MAY-1998; 98US-0084600P.

XX 28-MAY-1998; 98US-0087106P.

XX 02-JUN-1998; 98US-0087607P.

XX 02-JUN-1998; 98US-0087609P.

XX 02-JUN-1998; 98US-0087759P.

XX 03-JUN-1998; 98US-0087827P.

XX 04-JUN-1998; 98US-0088021P.

XX 04-JUN-1998; 98US-0088025P.

XX 04-JUN-1998; 98US-0088026P.

PR 04-JUN-1998; 98US-0088028P.
PR 04-JUN-1998; 98US-0088029P.
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PR 04-JUN-1998; 98US-0088033P.
PR 04-JUN-1998; 98US-0088326P.
PR 05-JUN-1998; 98US-0088167P.
PR 05-JUN-1998; 98US-0088202P.
PR 05-JUN-1998; 98US-0088212P.
PR 05-JUN-1998; 98US-0088217P.
PR 09-JUN-1998; 98US-0088655P.
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Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W; Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S; Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;

WPI; 2003-341980/32.
P-PSDB; ABO17856.

New secreted and transmembrane PRO nucleic acids, for treating inflammation, organ failure, atherosclerosis, cardiac injury, infertility, birth defects, premature aging, acquired immunodeficiency syndrome (AIDS), or cancer.

Claim 2; Fig 481; 660pp; English.

The invention describes an isolated nucleic acid (I) comprising, or which has 80 % sequence identity to, or the full-length coding sequence of, one of 275 nucleotide sequences, and which encodes a corresponding polypeptide selected from 275 amino acid sequences, where all sequences are given in the specification. The polypeptide encoded by (I) is used to detect PRO polypeptides, link a bioactive molecule to a cell expressing a PRO polypeptide, modulate a biological activity of a cell, stimulate the release of tumour necrosis factor (TNF)-alpha from human blood, modulate the uptake of glucose or free fatty acid by cells, stimulate or inhibit the proliferation or differentiation of cells or gene expression, stimulate the release of proteoglycans, stimulate the release of cytokine from peripheral blood mononuclear cells, inhibit the binding of A-peptide to factor VIIA, or detect the presence of tumour in a mammal. The nucleic acid and polypeptide encoded by it, are useful for treating inflammatory diseases, organ failure, atherosclerosis, cardiac injury, infertility, birth defects, premature aging, acquired immunodeficiency syndrome (AIDS), cancer, or diabetic complications. The nucleic acid is useful as hybridisation probes, in chromosome and gene mapping, and in generating antisense RNA or DNA. The polypeptides are useful as pharmaceuticals, diagnostics, biosensors or bioreactors. Both are useful in tissue typing. This sequence encodes a novel human secreted and transmembrane PRO polypeptide

Sequence 1346 BP; 457 A; 245 C; 237 G; 407 T; 0 U; 0 Other;

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Query Match      100.0%; Score 1346; DB 7; Length 1346;
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PR 28-AUG-2001; 2001US-00941992.

(GETH) GENENTECH INC.

PA Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
XX Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi JC, Gurney AL, Kljavin IJ, Napier MA, Pan J, Paoni NF;
PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;
XX Zhang Z;

DR WPI; 2003-288106/28.
DR P-PSDB; ABU60598.

XX New transmembrane polypeptides and nucleic acids encoding the
PT polypeptides, useful in gene therapy, in chromosome identification, as
PT chromosome markers, or in generating probes.

XX Claim 2; Fig 277; 650pp; English.

XX The invention discloses isolated PRO secreted/transmembrane polypeptides

CC comprising a sequence without signal peptide and the nucleic acid
CC encoding them. The polypeptides can be used to raise antibodies that
CC specifically bind to the PRO polypeptide, for linking a bioactive
CC molecule to a cell expressing a PRO protein and for modulating at least
CC one biological activity of a cell. The PRO polypeptides or
CC polynucleotides are also useful in gene therapy, in chromosome
CC identification, as chromosome markers, or in generating probes. The PRO
CC polypeptides are useful as molecular markers for protein electrophoresis,
CC and the isolated nucleic acids may be used for recombinantly expressing
CC those markers. The PRO polypeptides and nucleic acids may also be used in
CC tissue typing. Anti-PRO antibodies are useful in diagnostic assays for
CC PRO, and in affinity purification of PRO from recombinant cell culture or
CC natural sources. The sequences presented in ABX90083-ABX90468 are the
CC genes encoding, the primers amplifying and the probes detecting the PRO
CC polynucleotides of the invention. Note: The sequence data for this patent
CC is also available in electronic format from USPTO at
XX seqdata.uspto.gov/sequence.html

SQ Sequence 1346 BP; 457 A; 245 C; 237 G; 407 T; 0 U; 0 Other;

Query Match 100.0%; Score 1346; DB 7; Length 1346;
Best Local Similarity 100.0%; Pred. No. 1.6e-262;
Matches 1346; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GAAAGAAATGTTGGTCTCTTTTCTGTGACTGCCATTCACTGCTGAACCTCTGTCAA 60
DB 1 GAAAGAAATGTTGGTCTCTTTTCTGTGACTGCCATTCACTGCTGAACCTCTGTCAA 60
QY 61 CCAGGTGCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGAGATAAA 120
DB 61 CCAGGTGCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGAGATAAA 120
QY 121 GCATATGCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATG 180
DB 121 GCATATGCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATG 180
QY 181 AGAAAGTTCCCAACAGAGAACAGAAATTTCCCATGCTTCAAAAATACACACCTTCCCTGCT 240
DB 181 AGAAAGTTCCCAACAGAGAACAGAAATTTCCCATGCTTCAAAAATACACACCTTCCCTGCT 240
QY 241 CAGAGGGTATCATCTCTGTTTGTGTTACAGACCTTCCCAAAAATACACACCTTCCCTGCT 300
DB 241 CAGAGGGTATCATCTCTGTTTGTGTTACAGACCTTCCCAAAAATACACACCTTCCCTGCT 300
QY 301 GTTGAGGTGCAATCAGCCATAAGAATGAACAGAACCGGATCAACAATGCCCTTCTTTCTA 360
DB 301 GTTGAGGTGCAATCAGCCATAAGAATGAACAGAACCGGATCAACAATGCCCTTCTTTCTA 360
QY 361 AATGACCAAACTCTGGAATTTTAAATAATCCCTTCCACACTTGCACACCTTGGACCCCA 420
DB 361 AATGACCAAACTCTGGAATTTTAAATAATCCCTTCCACACTTGCACACCTTGGACCCCA 420
QY 421 TCTGTGCCCATCTGGATTATTATATTTTGGTGTGATATTTTGCATCATATAGTTGCAATT 480
DB 421 TCTGTGCCCATCTGGATTATTATATTTTGGTGTGATATTTTGCATCATATAGTTGCAATT 480
QY 481 GCACTACTGATTTTATCAGGGATCTGGCAACCTGAGAAAGAACAAAGAACCTATCTGAA 540
DB 481 GCACTACTGATTTTATCAGGGATCTGGCAACCTGAGAAAGAACAAAGAACCTATCTGAA 540
QY 541 GTGGATGACGCTGAAGATAACTGTGAAAACATGATCACAATTTGAAAATGGCATCCCTCT 600
DB 541 GTGGATGACGCTGAAGATAACTGTGAAAACATGATCACAATTTGAAAATGGCATCCCTCT 600
QY 601 GATCCCTTGCACATGAAGGGGGGCATATTATATGATGCCCTTCATGACAGAGGATGAGAGGC 660
DB 601 GATCCCTTGCACATGAAGGGGGGCATATTATATGATGCCCTTCATGACAGAGGATGAGAGGC 660
QY 661 TCACCCCTCTCTGAAGGGCTGTTGTTCTGCTCTCTCAAGAAATTAACATTTGTTCTGT 720
DB 661 TCACCCCTCTCTGAAGGGCTGTTGTTCTGCTCTCTCAAGAAATTAACATTTGTTCTGT 720
QY 721 GTGACTGTGAGCATCTCTGAATAACCAAGAGAGATCATATATTTTGTTCACCATCTT 780

Db 721 GTGACTGCTGAGCATCCTGAAATACCAAGACGAGATCATATATTTTGTTCACCATCTT 780
Qy 781 CTTTGTATAAATTTTGAATGTGCTTGAAAGTGAAAGCAATCAATTATACCCACCAAC 840
Db 781 CTTTGTATAAATTTTGAATGTGCTTGAAAGTGAAAGCAATCAATTATACCCACCAAC 840
Qy 841 ACCACTGAAATCATAGCTATTTCACGACTCAAAATATTCTAAATATTTTCTGCAGTA 900
Db 841 ACCACTGAAATCATAGCTATTTCACGACTCAAAATATTCTAAATATTTTCTGCAGTA 900
Qy 901 TAGTGATAAATGTGGTCATGTGGTATTGTAGTTATTGATTTAAGCAATTTTAGAATA 960
Db 901 TAGTGATAAATGTGGTCATGTGGTATTGTAGTTATTGATTTAAGCAATTTTAGAATA 960
Qy 961 AGATCAGGCATATGTATATATTTTTCACACTTCAAGACCTAAGGAAAAATAATTTTCCA 1020
Db 961 AGATCAGGCATATGTATATATTTTTCACACTTCAAGACCTAAGGAAAAATAATTTTCCA 1020
Qy 1021 GTGGAGAATACATATAATATGGTGTAGAAATCAATTGAAATGGATCCTTTTGCAGTCA 1080
Db 1021 GTGGAGAATACATATAATATGGTGTAGAAATCAATTGAAATGGATCCTTTTGCAGTCA 1080
Qy 1081 CTTATATCACTCTGTATATGACTAAGTAAACAAAAGTGAGAAGTAATTATTGTAATGGA 1140
Db 1081 CTTATATCACTCTGTATATGACTAAGTAAACAAAAGTGAGAAGTAATTATTGTAATGGA 1140
Qy 1141 TGGATAAAAAATGGAATTTACTCATATACAGGGTGGAAATTTTATCCTGTATCACACCAACA 1200
Db 1141 TGGATAAAAAATGGAATTTACTCATATACAGGGTGGAAATTTTATCCTGTATCACACCAACA 1200
Qy 1201 GTTGATTATATATTTTCTGAATATCAGCCCTTAATAGGACAAATCTATTTGTGACCAAT 1260
Db 1201 GTTGATTATATATTTTCTGAATATCAGCCCTTAATAGGACAAATCTATTTGTGACCAAT 1260
Qy 1261 TCTACAAATTTGTAAGTCCCAATCTGTGCTAACTTAATAAAGTAATAATCATCTCTTTT 1320
Db 1261 TCTACAAATTTGTAAGTCCCAATCTGTGCTAACTTAATAAAGTAATAATCATCTCTTTT 1320
Qy 1321 AAAAAAAAAAAAAAAAAAAAAA 1346
Db 1321 AAAAAAAAAAAAAAAAAAAAAA 1346

RESULT 11

ABX64194
ID ABX64194 standard; cDNA; 1346 BP.

AC ABX64194;

DT 26-FEB-2003 (first entry)

DE cDNA encoding human PRO1312 polypeptide.

XX Human; PRO polypeptide; secreted protein; transmembrane protein;
KW genetic disorder; antibacterial; immunosuppressive; transgenic;
KW gene therapy; gene; ss.

OS Homo sapiens.

XX US2002103125-A1.

PN 01-AUG-2002.

PD 20-NOV-2001; 2001US-00989731.

PF 16-JUN-1997; 97US-0049787P.

XX 17-OCT-1997; 97US-0062250P.

PR 05-NOV-1997; 97WO-US020069.

PR 12-NOV-1997; 97US-0065186P.

PR 13-NOV-1997; 97US-0065311P.

PR 24-NOV-1997; 97US-0066770P.

PR 25-FEB-1998; 98US-0075945P.

PR 20-MAR-1998; 98US-0078910P.
PR 28-APR-1998; 98US-0083322P.
PR 07-MAY-1998; 98US-0084600P.
PR 28-MAY-1998; 98US-0087106P.
PR 02-JUN-1998; 98US-0087607P.
PR 02-JUN-1998; 98US-0087609P.
PR 02-JUN-1998; 98US-0087759P.
PR 03-JUN-1998; 98US-0087827P.
PR 04-JUN-1998; 98US-0088021P.
PR 04-JUN-1998; 98US-0088025P.
PR 04-JUN-1998; 98US-0088026P.
PR 04-JUN-1998; 98US-0088028P.
PR 04-JUN-1998; 98US-0088029P.
PR 04-JUN-1998; 98US-0088030P.
PR 04-JUN-1998; 98US-0088033P.
PR 04-JUN-1998; 98US-0088326P.
PR 05-JUN-1998; 98US-0088167P.
PR 05-JUN-1998; 98US-0088202P.
PR 05-JUN-1998; 98US-0088212P.
PR 05-JUN-1998; 98US-0088217P.
PR 09-JUN-1998; 98US-0088655P.
PR 10-JUN-1998; 98US-0088734P.
PR 10-JUN-1998; 98US-0088738P.
PR 10-JUN-1998; 98US-0088742P.
PR 10-JUN-1998; 98US-0088810P.
PR 10-JUN-1998; 98US-0088824P.
PR 10-JUN-1998; 98US-0088826P.
PR 11-JUN-1998; 98US-0088858P.
PR 11-JUN-1998; 98US-0088861P.
PR 11-JUN-1998; 98US-0088876P.
PR 12-JUN-1998; 98US-0089105P.
PR 16-JUN-1998; 98US-0089440P.
PR 16-JUN-1998; 98US-0089512P.
PR 16-JUN-1998; 98US-0089514P.
PR 17-JUN-1998; 98US-0089532P.
PR 17-JUN-1998; 98US-0089538P.
PR 17-JUN-1998; 98US-0089598P.
PR 17-JUN-1998; 98US-0089599P.
PR 17-JUN-1998; 98US-0089600P.
PR 17-JUN-1998; 98US-0089653P.
PR 18-JUN-1998; 98US-0089801P.
PR 18-JUN-1998; 98US-0089907P.
PR 18-JUN-1998; 98US-0089908P.
PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98WO-US019437.
PR 07-OCT-1998; 98WO-US021141.
PR 01-DEC-1998; 98WO-US025108.
PR 05-JAN-1999; 99WO-US000106.
PR 08-MAR-1999; 99WO-US005028.
PR 02-JUN-1999; 99WO-US012252.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 30-NOV-1999; 99WO-US028313.
PR 01-DEC-1999; 99WO-US028301.
PR 01-DEC-1999; 99WO-US028634.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 06-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US004914.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 10-MAR-2000; 2000WO-US006319.
PR 15-MAR-2000; 2000WO-US006884.
PR 20-MAR-2000; 2000WO-US007377.
PR 30-MAR-2000; 2000WO-US008439.
PR 15-MAY-2000; 2000WO-US013358.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.

Db 1321 AAAAAAAAAAAAAAAAAAAAAAAAAA 1346

RESULT 12

ACA67234

ID ACA67234 standard; cDNA; 1346 BP.

XX ACA67234;

AC ACA67234;

XX 23-JUN-2003 (first entry)

XX cDNA encoding human PRO polypeptide #241.

DE Human; PRO polypeptide; secreted and transmembrane protein;

XX anti-PRO antibody; diagnostic assay; gene expression; diabetes;

KW bone disorder; cartilage disorder; rheumatoid arthritis; obesity;

KW sports injury; osteoarthritis; hyper-insulinaemia; hypo-insulinaemia;

KW hearing loss; coagulation disorder; stroke; heart attack; cardiac;

KW antidiabetic; anorectic; vulnery; antiarthritic; osteopathic;

KW antirheumatic; auditory; cerebroprotective; angiogenic; gene; ss.

XX Homo sapiens.

OS US2003004311-A1.

PN 02-JAN-2003.

XX 19-DEC-2001; 2001US-00028072.

XX 18-JUN-1997; 97US-0049911P.

PR 26-AUG-1997; 97US-0056974P.

PR 17-SEP-1997; 97US-0059113P.

PR 17-SEP-1997; 97US-0059115P.

PR 17-SEP-1997; 97US-0059117P.

PR 17-SEP-1997; 97US-0059122P.

PR 17-SEP-1997; 97US-0059184P.

PR 18-SEP-1997; 97US-0059263P.

PR 19-SEP-1997; 97US-0059352P.

PR 19-SEP-1997; 97US-0059588P.

PR 24-SEP-1997; 97US-0059836P.

PR 17-OCT-1997; 97US-0062250P.

PR 17-OCT-1997; 97US-0062285P.

PR 17-OCT-1997; 97US-0062287P.

PR 17-OCT-1997; 97US-0063755P.

PR 24-OCT-1997; 97US-0062814P.

PR 24-OCT-1997; 97US-0062816P.

PR 24-OCT-1997; 97US-0063045P.

PR 24-OCT-1997; 97US-0063082P.

PR 24-OCT-1997; 97US-0063127P.

PR 27-OCT-1997; 97US-0063327P.

PR 27-OCT-1997; 97US-0063329P.

PR 28-OCT-1997; 97US-0063550P.

PR 28-OCT-1997; 97US-0063561P.

PR 29-OCT-1997; 97US-0063704P.

PR 29-OCT-1997; 97US-0063733P.

PR 29-OCT-1997; 97US-0063735P.

PR 29-OCT-1997; 97US-0063738P.

PR 03-NOV-1997; 97US-0064248P.

PR 07-NOV-1997; 97US-0064809P.

PR 12-NOV-1997; 97US-0065186P.

PR 17-NOV-1997; 97US-0065846P.

PR 21-NOV-1997; 97US-0066364P.

PR 24-NOV-1997; 97US-0066453P.

PR 24-NOV-1997; 97US-0066511P.

PR 24-NOV-1997; 97US-0066770P.

PR 11-DEC-1997; 97US-0069212P.

PR 11-DEC-1997; 97US-0069278P.

PR 11-DEC-1997; 97US-0069334P.

PR 16-DEC-1997; 97US-0069694P.

PR 23-JAN-1998; 98US-0072320P.

PR 04-FEB-1998; 98US-0073612P.

PR 09-FEB-1998; 98US-0074086P.

PR 09-FEB-1998; 98US-0074092P.

PR 12-MAR-1998; 98US-0077791P.

PR 20-MAR-1998; 98US-0078910P.

PR 25-MAR-1998; 98US-0079294P.

PR 27-MAR-1998; 98US-0079663P.

PR 27-MAR-1998; 98US-0079728P.

PR 31-MAR-1998; 98US-0080165P.

PR 12-JUN-1998; 98WO-US012456.

PR 14-JUL-1998; 98WO-US014552.

PR 28-AUG-1998; 98WO-US017888.

PR 10-SEP-1998; 98WO-US018824.

PR 14-SEP-1998; 98WO-US019093.

PR 14-SEP-1998; 98WO-US019094.

PR 14-SEP-1998; 98WO-US019177.

PR 16-SEP-1998; 98WO-US019330.

PR 17-SEP-1998; 98WO-US019437.

PR 07-OCT-1998; 98WO-US021141.

PR 29-OCT-1998; 98WO-US022991.

PR 29-OCT-1998; 98WO-US022992.

PR 20-NOV-1998; 98WO-US024855.

PR 01-DEC-1998; 98WO-US025108.

PR 05-JAN-1999; 99WO-US000106.

PR 08-MAR-1999; 99WO-US005028.

PR 10-MAR-1999; 99WO-US005190.

PR 20-APR-1999; 99WO-US008615.

PR 14-MAY-1999; 99WO-US010733.

PR 02-JUN-1999; 99WO-US012252.

PR 01-SEP-1999; 99WO-US020111.

PR 08-SEP-1999; 99WO-US020594.

PR 13-SEP-1999; 99WO-US020944.

PR 15-SEP-1999; 99WO-US021090.

PR 15-SEP-1999; 99WO-US021547.

PR 05-OCT-1999; 99WO-US023089.

PR 29-NOV-1999; 99WO-US028214.

PR 30-NOV-1999; 99WO-US028313.

PR 30-NOV-1999; 99WO-US028409.

PR 01-DEC-1999; 99WO-US028301.

PR 01-DEC-1999; 99WO-US028634.

PR 02-DEC-1999; 99WO-US028551.

PR 02-DEC-1999; 99WO-US028564.

PR 02-DEC-1999; 99WO-US028565.

PR 16-DEC-1999; 99WO-US030095.

PR 20-DEC-1999; 99WO-US030911.

PR 20-DEC-1999; 99WO-US030999.

PR 30-DEC-1999; 99WO-US031243.

PR 30-DEC-1999; 99WO-US031274.

PR 05-JAN-2000; 2000WO-US000219.

PR 06-JAN-2000; 2000WO-US000277.

PR 06-JAN-2000; 2000WO-US000376.

PR 11-FEB-2000; 2000WO-US003565.

PR 18-FEB-2000; 2000WO-US004341.

PR 18-FEB-2000; 2000WO-US004342.

PR 22-FEB-2000; 2000WO-US004414.

PR 24-FEB-2000; 2000WO-US004914.

PR 24-FEB-2000; 2000WO-US005004.

PR 01-MAR-2000; 2000WO-US005601.

PR 02-MAR-2000; 2000WO-US005746.

(GETH) GENENTECH INC.

XX Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;
XX Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
XX Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
XX WPI; 2003-352836/33.
XX P-PSDB; ABU81110.

XX New isolated PRO polypeptide useful for treating diabetes, rheumatoid
XX arthritis, sports injuries, obesity, hearing loss in mammals, stroke, or
XX heart attack.

Claim 2; Fig 481; 643pp; English.

The present invention relates to the isolation of novel human PRO

CC polypeptides, and the polynucleotide sequences encoding them. The PRO
CC polypeptides are secreted and transmembrane proteins. The PRO
CC polypeptides and polynucleotides are useful for preparing a medicament
CC useful in the treatment of diabetes, bone and/or cartilage disorders
CC (e.g. rheumatoid arthritis, sports injuries, osteoarthritis), obesity,
CC hyper- or hypo-insulinaemia, hearing loss, and coagulation disorders
CC (e.g. stroke, heart attack). Anti-PRO antibodies are useful in diagnostic
CC assays for PRO, by detecting its expression in specific cells, tissues or
CC serum, and for affinity purification of PRO from recombinant cell culture
CC or natural sources. ACA66994-ACA67268 represent cDNA sequences encoding
CC the human PRO polypeptides of the invention. Note: The sequence data for
CC this patent was obtained in electronic format directly from the USPTO web
CC site at seqdata.uspto.gov/psipsDIDEntry.html
XX

SQ Sequence 1346 BP; 457 A; 245 C; 237 G; 407 T; 0 U; 0 Other;

Query Match 100.0%; Score 1346; DB 7; Length 1346;
Best Local Similarity 100.0%; Pred. No. 1.6e-262;
Matches 1346; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAGAATGTTGGCTGCTCTTTTCTGGTGACTGCCATTCAATGCTGAACCTCTGTCAA 60
DB |||||||
QY 1 GAAGAATGTTGGCTGCTCTTTTCTGGTGACTGCCATTCAATGCTGAACCTCTGTCAA 60
DB |||||||
QY 61 CCAGGTGCAGAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAA 120
DB |||||||
QY 61 CCAGGTGCAGAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAA 120
DB |||||||
QY 121 GCATATGCTGGGATACCAATGAAGATACCTCTTCAAGCGATGGTAGCTTCTCCATG 180
DB |||||||
QY 121 GCATATGCTGGGATACCAATGAAGATACCTCTTCAAGCGATGGTAGCTTCTCCATG 180
DB |||||||
QY 181 AGAAAGTTCCCAACAGAGAGAACAGAAATTTCCCATGCTCCTACTTTGCAATGTAACC 240
DB |||||||
QY 181 AGAAAGTTCCCAACAGAGAGAACAGAAATTTCCCATGCTCCTACTTTGCAATGTAACC 240
DB |||||||
QY 241 CAGAGGGTATCATTTCTGGTTTGTGGTTACAGACCCCTCAAAAATACACACCCCTTCTGCT 300
DB |||||||
QY 241 CAGAGGGTATCATTTCTGGTTTGTGGTTACAGACCCCTCAAAAATACACACCCCTTCTGCT 300
DB |||||||
QY 301 GTTGAGGTGCAATCAGCCATAAGATGAACAGACCGGATCAACAAATGCCCTTCTTCTA 360
DB |||||||
QY 301 GTTGAGGTGCAATCAGCCATAAGATGAACAGACCGGATCAACAAATGCCCTTCTTCTA 360
DB |||||||
QY 361 AATGACCAAACTCTGGAAATTTTAAATAATCCCTTCCACACTTGACACCCATGGACCCA 420
DB |||||||
QY 361 AATGACCAAACTCTGGAAATTTTAAATAATCCCTTCCACACTTGACACCCATGGACCCA 420
DB |||||||
QY 421 TCTGTGCCCATCTGGATTATTAATTTGGTGTGATATTTTGCATCATATAGTTGCAATT 480
DB |||||||
QY 421 TCTGTGCCCATCTGGATTATTAATTTGGTGTGATATTTTGCATCATATAGTTGCAATT 480
DB |||||||
QY 481 GCATCTACTGATTTTATCAGGGATCTGGCAACGTCAGAGAAAGAACAAAGAACCAATCTGAA 540
DB |||||||
QY 481 GCATCTACTGATTTTATCAGGGATCTGGCAACGTCAGAGAAAGAACAAAGAACCAATCTGAA 540
DB |||||||
QY 541 GTGGATGACGCTGAGATAAGTGTGAAAACATGATCACAATTTGAAATGGCATCCCTCT 600
DB |||||||
QY 541 GTGGATGACGCTGAGATAAGTGTGAAAACATGATCACAATTTGAAATGGCATCCCTCT 600
DB |||||||
QY 601 GATCCCTGGACATGAAGGGGGGCATATTAATGATGCTTCAATGACAGAGGATGAGAGGC 660
DB |||||||
QY 601 GATCCCTGGACATGAAGGGGGGCATATTAATGATGCTTCAATGACAGAGGATGAGAGGC 660
DB |||||||
QY 661 TCACCCCTCTCTGAAGGGCTGTTCTGCTTCCCAAGAAATTAACATTTGTTCTGT 720
DB |||||||
QY 661 TCACCCCTCTCTGAAGGGCTGTTCTGCTTCCCAAGAAATTAACATTTGTTCTGT 720
DB |||||||
QY 721 GTGACTGCTGACCATCTGAAATACCAAGAGCAGATCATATATTTTGTTCACCATCTT 780
DB |||||||
QY 721 GTGACTGCTGACCATCTGAAATACCAAGAGCAGATCATATATTTTGTTCACCATCTT 780
DB |||||||
QY 781 CTTTGTATAAATTTTGAATGTGCTTGAAGTGAAGCAATCAATTATACCCCAAC 840

DB 781 CTTTGTATAAATTTTGAATGTGCTTGAAGTGAAGCAATCAATTATACCCCAAC 840
QY 841 ACCACTGAAATCATAGCTATTACAGACTCAAAATATTCTAAATATTTTCTGACAGTA 900
DB |||||||
QY 841 ACCACTGAAATCATAGCTATTACAGACTCAAAATATTCTAAATATTTTCTGACAGTA 900
DB |||||||
QY 901 TAGTGATAAATGCTGCTCATGTGGTATTGTAGTTATTGAATTAAGCAATTTTAGAATA 960
DB |||||||
QY 901 TAGTGATAAATGCTGCTCATGTGGTATTGTAGTTATTGAATTAAGCAATTTTAGAATA 960
DB |||||||
QY 961 AGATCAGGCATATGTATATATTTTTCACACTTCAAGAGCTCAAGGAAATAAATTTTCCA 1020
DB |||||||
QY 961 AGATCAGGCATATGTATATATTTTTCACACTTCAAGAGCTCAAGGAAATAAATTTTCCA 1020
DB |||||||
QY 1021 GTGGAGAAATACATATAATATGGTGTAGAAATCAATTGAAATGGATCCTTTTGGACGATCA 1080
DB |||||||
QY 1021 GTGGAGAAATACATATAATATGGTGTAGAAATCAATTGAAATGGATCCTTTTGGACGATCA 1080
DB |||||||
QY 1081 CTTATATCACTCTGTATATGACTAAGTAAACAAAAGTGAGAAAGTAATTAATTTGTAATGGA 1140
DB |||||||
QY 1081 CTTATATCACTCTGTATATGACTAAGTAAACAAAAGTGAGAAAGTAATTAATTTGTAATGGA 1140
DB |||||||
QY 1141 TGGATAAATAATGGAATTAATCTATATACAGGGTGGAAATTTTATCTGTATCACACCAACA 1200
DB |||||||
QY 1141 TGGATAAATAATGGAATTAATCTATATACAGGGTGGAAATTTTATCTGTATCACACCAACA 1200
DB |||||||
QY 1201 GTTGATATATATTTTCTGAATATCAGCCCTTAATAGGCAATTTCTATTTGTGACCATT 1260
DB |||||||
QY 1201 GTTGATATATATTTTCTGAATATCAGCCCTTAATAGGCAATTTCTATTTGTGACCATT 1260
DB |||||||
QY 1261 TCTACAAATTTGTAAGTCCAAATCTGTGCTAACTTAATAAGTAATAATCATCTCTTTT 1320
DB |||||||
QY 1261 TCTACAAATTTGTAAGTCCAAATCTGTGCTAACTTAATAAGTAATAATCATCTCTTTT 1320
DB |||||||
QY 1321 AAAAAAAAAAAAAAAAAAAAAA 1346
DB |||||||
QY 1321 AAAAAAAAAAAAAAAAAAAAAA 1346
DB |||||||

RESULT 13

ACA64416

ID ACA64416 standard; cDNA; 1346 BP.

XX ACA64416;

AC ACA64416;

XX 17-JUN-2003 (first entry)

XX Novel human secreted and transmembrane protein PRO1312 cDNA.

XX Human; secreted and transmembrane protein; cytostatic; anti-HIV;
KW virucide; hepatotropic; antiinflammatory; neuroprotective; gene therapy;
KW PRO; pharmaceutical; diagnostic; biosensor; bioreactor; malignancy;
KW cancer; ovarian cancer; colorectal cancer; Kaposi's sarcoma; leukaemia;
KW lymphoma; hepatitis B; multiple sclerosis; Crohn's disease;
KW drug screening; gene; ss.

OS Homo sapiens.

XX US2003003531-A1.

PD 02-JAN-2003.

PF 19-NOV-2001; 2001US-00989734.

XX 16-JUN-1997; 97US-0049787P.

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PR 04-JUN-1998; 98US-0088030P.
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PR 04-JUN-1998; 98US-0088326P.
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PR 10-JUN-1998; 98US-0088734P.
PR 10-JUN-1998; 98US-0088738P.
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PR 10-JUN-1998; 98US-0088810P.
PR 10-JUN-1998; 98US-0088824P.
PR 10-JUN-1998; 98US-0088826P.
PR 11-JUN-1998; 98US-0088858P.
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PR 08-MAR-1999; 99WO-US005028.
PR 02-JUN-1999; 99WO-US012252.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 30-NOV-1999; 99WO-US028313.
PR 01-DEC-1999; 99WO-US028301.
PR 01-DEC-1999; 99WO-US028634.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US00376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US004914.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 10-MAR-2000; 2000WO-US006319.
PR 15-MAR-2000; 2000WO-US006884.
PR 20-MAR-2000; 2000WO-US007377.
PR 30-MAR-2000; 2000WO-US008439.
PR 15-MAY-2000; 2000WO-US013358.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.

PR 28-JUL-2000; 2000WO-US020710.
PR 11-AUG-2000; 2000WO-US022031.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000WO-US030952.
PR 01-DEC-2000; 2000WO-US032678.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-JUN-2001; 2001WO-US017800.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 28-AUG-2001; 2001US-00941992.
XX
PA (GETH) GENENTECH INC.
XX
XX
PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
PI Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi JC, Gurney AL, Kljavin IJ, Napier MA, Pan J, Paoni NF;
PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;
PI Zhang Z;
XX
DR WPI; 2003-352829/33.
DR P-PSDB; ABU72565.
XX
PT New genes and secreted and transmembrane polypeptides (e.g. PRO183 or
PT PRO184), useful for treating or diagnosing e.g. ovarian cancer, Kaposi's
PT sarcoma, leukemia, lymphoma, hepatitis B, multiple sclerosis or Crohn's
PT disease.
XX
PS Claim 1; Fig 277; 663pp; English.
XX
CC The invention describes a new isolated nucleic acid molecule comprising
CC the full length coding sequence of the DNA deposited with the American
CC Type Culture Collection (e.g. ATCC Deposit No. 209621, 552-PTA, 819-PTA,
CC 209439, 203135, etc); or a sequence with at least 80% identity to a DNA
CC encoding a PRO polypeptide. The PRO polypeptides or polynucleotides are
CC useful as pharmaceuticals, diagnostics, biosensors or bioreactors. These
CC are particularly useful for detecting or treating e.g. malignancies or
CC cancers (e.g. ovarian cancer, colorectal cancer, Kaposi's sarcoma,
CC leukaemia or lymphoma), hepatitis B, multiple sclerosis, or Crohn's
CC disease in mammals. The PRO polypeptides are useful in drug screening,
CC particularly as targets for therapeutic intervention in these diseases,
CC and in the diagnostic determination of the presence of these diseases.
CC The PRO polypeptides are also useful as molecular weight markers, or for
CC chromosome identification. The PRO genes are useful as hybridisation
CC probes, or for screening libraries of human cDNA, genomic DNA or mRNA.
CC The PRO genes may also be used in gene therapy, particularly for
CC replacing a defective gene. This sequence encodes a novel human secreted
CC and transmembrane PRO polypeptide
XX
SQ Sequence 1346 BP; 457 A; 245 C; 237 G; 407 T; 0 U; 0 Other;

Query Match 100.0%; Score 1346; DB 7; Length 1346;
Best Local Similarity 100.0%; Pred. No. 1.6e-262;
Matches 1346; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAAGAATGTTGGTGCTCTTTTCTGGTGACTGCCATTGCTGAACTCTGTCAA 60
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||
1 GAAAGAATGTTGGTGCTCTTTTCTGGTGACTGCCATTGCTGAACTCTGTCAA 60

QY 61 CCAGGTGCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAA 120
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||
61 CCAGGTGCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAA 120

QY 121 GCATATGCTGGGATACCAATGAAGATACCTCTTCAAAGCGATGGTAGTTTCTCCATG 180
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||
121 GCATATGCTGGGATACCAATGAAGATACCTCTTCAAAGCGATGGTAGTTTCTCCATG 180

QY 181 AGAAAAGTCCCAACAGAGAAGCAACAGAAAATTTCCCATGTCCTACTTTGCAATGTAACC 240
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||
181 AGAAAAGTCCCAACAGAGAAGCAACAGAAAATTTCCCATGTCCTACTTTGCAATGTAACC 240

QY 241 CAGAGGGTATCAITCTGCTTGTGGTTACAGACCCCTTCAAAAAAATCACACCCCTTCTGCT 300

Db 241 ||||| CAGAGGGTATCATCTGTTTGGTTACAGACCCTTCAAAAAATCACACCTTCCTGCT 300
Qy 301 GTTGAGGTGCAATCAGCCATAAGAAATGAACAAGAACCGGATCAACAATGCCCTTTCTTA 360
Db 301 GTTGAGGTGCAATCAGCCATAAGAAATGAACAAGAACCGGATCAACAATGCCCTTTCTTA 360
Qy 361 AATGACCAAACTCTGGAAATTTTAAAAATCCCTTCCACACTTGCACCAACCCATGGACCCA 420
Db 361 AATGACCAAACTCTGGAAATTTTAAAAATCCCTTCCACACTTGCACCAACCCATGGACCCA 420
Qy 421 TCTGTGCCCATCTGGATTTATATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATT 480
Db 421 TCTGTGCCCATCTGGATTTATATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATT 480
Qy 481 GCACTACTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCCATCTGAA 540
Db 481 GCACTACTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCCATCTGAA 540
Qy 541 GTGGATGACCGCTGAAGATAAGTGTGAAACCATGATCACAATTTGAAATGGCATCCCTCT 600
Db 541 GTGGATGACCGCTGAAGATAAGTGTGAAACCATGATCACAATTTGAAATGGCATCCCTCT 600
Qy 601 GATCCCTCGACATGAAGGGGGCATATTAATGATGCCCTTCATGACAGAGGATGAGAGGC 660
Db 601 GATCCCTCGACATGAAGGGGGCATATTAATGATGCCCTTCATGACAGAGGATGAGAGGC 660
Qy 661 TCACCCCTCTCTGAAGGGCTGTTGTTCTGCTTCTCAAGAAATTAACAATTTGTTCTGT 720
Db 661 TCACCCCTCTCTGAAGGGCTGTTGTTCTGCTTCTCAAGAAATTAACAATTTGTTCTGT 720
Qy 721 GTGACTGCTGAGCATCTGAATPACCAAGAGCAGATCATATATTTGTTTCACCATCTT 780
Db 721 GTGACTGCTGAGCATCTGAATPACCAAGAGCAGATCATATATTTGTTTCACCATCTT 780
Qy 781 CTTTGTAAATAAATTTGAATGTGCTTGAAGTGAAAGCAATCAATATATACCCACCAAC 840
Db 781 CTTTGTAAATAAATTTGAATGTGCTTGAAGTGAAAGCAATCAATATATACCCACCAAC 840
Qy 841 ACCACTGAAATCATAAAGCTATTACGACTCAAAATATTCTAAATATTTTCTGACAGTA 900
Db 841 ACCACTGAAATCATAAAGCTATTACGACTCAAAATATTCTAAATATTTTCTGACAGTA 900
Qy 901 TAGTGATATAATGTGGTCAATGGTATTGTTAGTATTGATTTAAGCATTTTGTAGAAATA 960
Db 901 TAGTGATATAATGTGGTCAATGGTATTGTTAGTATTGATTTAAGCATTTTGTAGAAATA 960
Qy 961 AGATCAGGCATATATATATTTTTCACACTTCAAGACCTAAGGAAATAAATTTTCCA 1020
Db 961 AGATCAGGCATATATATATTTTTCACACTTCAAGACCTAAGGAAATAAATTTTCCA 1020
Qy 1021 GTGGAGAAATACATATAATATGTTGAGTAAATCATTTGAAATGGATCTTTTTCAGCATCA 1080
Db 1021 GTGGAGAAATACATATAATATGTTGAGTAAATCATTTGAAATGGATCTTTTTCAGCATCA 1080
Qy 1081 CTTATATCACTCTGTATATGACTAAGTAACAAAGTGAGAGTAATTTTGTAAATGGA 1140
Db 1081 CTTATATCACTCTGTATATGACTAAGTAACAAAGTGAGAGTAATTTTGTAAATGGA 1140
Qy 1141 TGGATAAAAATGGAATTTACTCATATACAGGGTGAATTTTATCTCTGTTATCACACCAACA 1200
Db 1141 TGGATAAAAATGGAATTTACTCATATACAGGGTGAATTTTATCTCTGTTATCACACCAACA 1200
Qy 1201 GTTGATTATATATTTCTGAATATCAGCCCTAATAGGACAATTTCTATTTGTTGACCAATT 1260
Db 1201 GTTGATTATATATTTCTGAATATCAGCCCTAATAGGACAATTTCTATTTGTTGACCAATT 1260
Qy 1261 TCTACAATTTGTAAAGTCCCAATCTGTGCTAACTTAATAAGTAATAATCATCTCTTTTT 1320
Db 1261 TCTACAATTTGTAAAGTCCCAATCTGTGCTAACTTAATAAGTAATAATCATCTCTTTTT 1320
Qy 1321 AAAAAAAAAAAAAAAAAAAAAA 1346
|||||

Db 1321 AAAAAAAAAAAAAAAAAAAAAA 1346
RESULT 14
ID ACA03843 standard; cDNA; 1346 BP.
XX
AC ACA03843;
XX
DT 23-MAY-2003 (first entry)
XX
DE cDNA encoding human PRO polypeptide #241.
XX
KW Human; PRO polypeptide; secreted and transmembrane protein;
KW tumour necrosis factor-alpha; TNF-alpha; blood; proliferation;
KW differentiation; chondrocyte; tumour; genetic disorder; cytostatic; gene;
KW ss.
XX
OS Homo sapiens.
XX
PN US2003036180-A1.
XX
PD 20-FEB-2003.
XX
PF 09-MAY-2002; 2002US-00143114.
XX
PR 31-MAR-1997; 97WO-US005230.
PR 12-JUN-1998; 98WO-US012456.
PR 14-JUL-1998; 98WO-US014552.
PR 28-AUG-1998; 98WO-US017888.
PR 10-SEP-1998; 98WO-US018824.
PR 14-SEP-1998; 98WO-US019093.
PR 14-SEP-1998; 98WO-US019094.
PR 14-SEP-1998; 98WO-US019177.
PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98WO-US019437.
PR 07-OCT-1998; 98WO-US021141.
PR 29-OCT-1998; 98WO-US022991.
PR 29-OCT-1998; 98WO-US022992.
PR 20-NOV-1998; 98WO-US024855.
PR 01-DEC-1998; 98WO-US025108.
PR 05-JAN-1999; 99WO-US000106.
PR 08-MAR-1999; 99WO-US005028.
PR 10-MAR-1999; 99WO-US005190.
PR 20-APR-1999; 99WO-US008615.
PR 14-MAY-1999; 99WO-US010733.
PR 02-JUN-1999; 99WO-US012252.
PR 01-SEP-1999; 99WO-US020111.
PR 08-SEP-1999; 99WO-US020594.
PR 13-SEP-1999; 99WO-US020944.
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PR 15-SEP-1999; 99WO-US021547.
PR 05-OCT-1999; 99WO-US023089.
PR 29-NOV-1999; 99WO-US028214.
PR 30-NOV-1999; 99WO-US028313.
PR 30-NOV-1999; 99WO-US028409.
PR 01-DEC-1999; 99WO-US028301.
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PR 02-DEC-1999; 99WO-US028564.
PR 02-DEC-1999; 99WO-US028565.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 20-DEC-1999; 99WO-US030999.
PR 22-DEC-1999; 99WO-US030720.
PR 30-DEC-1999; 99WO-US031243.
PR 30-DEC-1999; 99WO-US031274.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000277.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 18-FEB-2000; 2000WO-US004342.

PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US004914.
PR 24-FEB-2000; 2000WO-US005004.
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005746.
PR 02-MAR-2000; 2000WO-US005841.
PR 10-MAR-2000; 2000WO-US006319.
PR 15-MAR-2000; 2000WO-US006884.
PR 20-MAR-2000; 2000WO-US007377.
PR 21-MAR-2000; 2000WO-US007532.
PR 30-MAR-2000; 2000WO-US008439.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 11-AUG-2000; 2000WO-US022031.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000WO-US030952.
PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001US-00796498.
PR 28-FEB-2001; 2001WO-US005520.
PR 01-MAR-2001; 2001WO-US006666.
PR 09-MAR-2001; 2001US-00802706.
PR 14-MAR-2001; 2001US-00808689.
PR 22-MAR-2001; 2001US-00816744.
PR 05-APR-2001; 2001US-00828366.
PR 10-MAY-2001; 2001US-00854208.
PR 10-MAY-2001; 2001US-00854280.
PR 18-MAY-2001; 2001US-00860216.
PR 25-MAY-2001; 2001US-00866028.
PR 25-MAY-2001; 2001US-00866034.
PR 25-MAY-2001; 2001WO-US017092.
PR 01-JUN-2001; 2001US-00872035.
PR 01-JUN-2001; 2001WO-US017800.
PR 05-JUN-2001; 2001US-00874503.
PR 14-JUN-2001; 2001US-00882636.
PR 19-JUN-2001; 2001US-00886342.
PR 20-JUN-2001; 2001WO-US019692.
PR 21-JUN-2001; 2001US-00887879.
PR 22-JUN-2001; 2001WO-US020116.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 18-JUL-2001; 2001US-00908827.
PR 06-AUG-2001; 2001US-00924419.
PR 09-AUG-2001; 2001US-00927796.
PR 16-AUG-2001; 2001US-00931836.
PR 19-DEC-2001; 2001US-00028072.

(GETH) GENENTECH INC.

PI Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;
PI Geritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;

XX WPI; 2003-332040/31.

DR P-PSDB; ABU66810.

XX
PT New secreted and transmembrane PRO nucleic acids, useful for gene
PT therapy, in chromosome and gene mapping, as chromosome markers, in tissue
PT typing, and in chromosome identification.

XX Claim 2; Fig 481; 660pp; English.

XX The present invention relates to the isolation of novel human PRO
CC polypeptides, and the polynucleotide sequences encoding them. The PRO
CC polypeptides are secreted and transmembrane proteins. The PRO
CC polypeptides are useful for detecting other PRO polypeptides, for linking
CC bioactive molecules to cells expressing PRO polypeptides, for modulating

CC biological activities of cells expressing PRO polypeptides, and for
CC identifying agonists or antagonists. The PRO polypeptides are useful for
CC for stimulating the release of tumour necrosis factor (TNF)-alpha from
CC human blood, for stimulating the proliferation or differentiation of
CC chondrocytes, and detecting the presence of tumours. The polynucleotide
CC sequences encoding PRO polypeptides are useful as hybridisation probes,
CC in chromosome and gene mapping, in the generation of antisense RNA and
CC DNA, in the preparation of PRO polypeptides, for generating transgenic
CC animals or knockout animals, for the genetic analysis of individuals with
CC genetic disorders, and in gene therapy. ACA03603-ACA03877 represent cDNAs
CC encoding the human PRO polypeptides of the invention. Note: The sequence
CC data for this patent was obtained in electronic format directly from the
CC USPTO web site at seqdata.uspto.gov/psipsdIDEntry.html

XX
SQ Sequence 1346 BP; 457 A; 245 C; 237 G; 407 T; 0 U; 0 Other;

Query Match 100.0%; Score 1346; DB 7; Length 1346;

Best Local Similarity 100.0%; Pred. No. 1.6e-262;

Matches 1346; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAAGAAATGTTGGGCTGCTCTTTTCTGGTGACCTGACATTCAGCTGAACTCTGTCAA 60
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 1 GAAAGAAATGTTGGGCTGCTCTTTTCTGGTGACCTGACATTCAGCTGAACTCTGTCAA 60
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 61 CCAGGTGCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAA 120
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 61 CCAGGTGCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAA 120
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 121 GCATATGCTGGGATACCAATGAAGATACCTCTTCAAAGCGATGGTAGCTTCTCCATG 180
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 121 GCATATGCTGGGATACCAATGAAGATACCTCTTCAAAGCGATGGTAGCTTCTCCATG 180
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 181 AGAAAGTTCCCAACAGAGAAGCAACAGAAAATTTCCCATGTCTACTTTTGCATGTAACC 240
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 181 AGAAAGTTCCCAACAGAGAAGCAACAGAAAATTTCCCATGTCTACTTTTGCATGTAACC 240
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 241 CAGAGGTATCAATCTGTTGTTGTGTACAGACCCCTTCAAAAAATCACACCCCTTCTCTGCT 300
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 241 CAGAGGTATCAATCTGTTGTTGTGTACAGACCCCTTCAAAAAATCACACCCCTTCTCTGCT 300
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 301 GTTGAGGTGCAATCAGCCATAAGAAATGAACAAAGAACCGGATCAACAAATGCTTCTTCTA 360
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 301 GTTGAGGTGCAATCAGCCATAAGAAATGAACAAAGAACCGGATCAACAAATGCTTCTTCTA 360
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 361 AATGACCAAACTCTGGAATTTTAAATCCCTTCCACACTTGACCCATGGACCCA 420
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 361 AATGACCAAACTCTGGAATTTTAAATCCCTTCCACACTTGACCCATGGACCCA 420
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 421 TCTGTGCCCATCTGGATTAATATATTTGGTGATATTTTGCATCATCATGATGCAATT 480
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 421 TCTGTGCCCATCTGGATTAATATATTTGGTGATATTTTGCATCATCATGATGCAATT 480
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 481 GCACTACTGATTTTATCAGGGATCTGGCAACGTTAGAGAAAGAAACCAAGAACCATCTGAA 540
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 481 GCACTACTGATTTTATCAGGGATCTGGCAACGTTAGAGAAAGAAACCAAGAACCATCTGAA 540
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 541 GTGGATGACGCTGAAGATAAGTGTGAAAACATGATCACAATTTGAAAATGGCATCCCTCT 600
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 541 GTGGATGACGCTGAAGATAAGTGTGAAAACATGATCACAATTTGAAAATGGCATCCCTCT 600
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 601 GATCCCTGGACATGAAGGGGGGCGCATATTAATGATGCTTTCATGACAGAGGATGAGAGGC 660
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 601 GATCCCTGGACATGAAGGGGGGCGCATATTAATGATGCTTTCATGACAGAGGATGAGAGGC 660
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 661 TCACCCCTCTCTGAAGGGCTGTTGTTCTGCTTCCCAAGAAATTAACATTTGTTCTGT 720
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 661 TCACCCCTCTCTGAAGGGCTGTTGTTCTGCTTCCCAAGAAATTAACATTTGTTCTGT 720
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 721 GTGACTGTGAGCATCTGAAATACCAAGAGCAGATCATATATTTTGTTCACCATCTT 780
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 721 GTGACTGTGAGCATCTGAAATACCAAGAGCAGATCATATATTTTGTTCACCATCTT 780
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 781 CTTTGTGTAATAAATTTGATGTGCTTGAAGTGAAGCAATCAATTATACCCCAAC 840

Db	781	CTTTTGTAAATAATTTTGAATGTGCTTGAAGTGAAGAGCAATCAATTATATACCCACCAAC	840	PR 10-SEP-1998;	98WO-US018824
Qy	841	ACCACTGAAATCATAGCTATTTCACGACTCAAAAATATTTCTAAAATATTTTCTGACAGTA	900	PR 14-SEP-1998;	98WO-US019093
Db	841	ACCACTGAAATCATAGCTATTTCACGACTCAAAAATATTTCTAAAATATTTTCTGACAGTA	900	PR 14-SEP-1998;	98WO-US019094
Qy	901	TAGTGTATAAATGTGGTCAATGCTGATTTTCTAGTTATTTGATTTTAAAGCATTTTGTAGAAATA	960	PR 16-SEP-1998;	98WO-US019177
Db	901	TAGTGTATAAATGTGGTCAATGCTGATTTTCTAGTTATTTGATTTTAAAGCATTTTGTAGAAATA	960	PR 17-SEP-1998;	98WO-US019330
Qy	961	AGATCAGGCATATGTATATATTTTTCACACTTCAAAGACCTTAAGGAAAAATAAATTTTCTCA	1020	PR 07-OCT-1998;	98WO-US019437
Db	961	AGATCAGGCATATGTATATATTTTTCACACTTCAAAGACCTTAAGGAAAAATAAATTTTCTCA	1020	PR 07-OCT-1998;	98WO-US021141
Qy	1021	GTGGAGAAATACATATATATATTTTGTAGTAATCATTTGAAATGGATCCTTTTGTACGATCA	1080	PR 29-OCT-1998;	98WO-US022991
Db	1021	GTGGAGAAATACATATATATATTTTGTAGTAATCATTTGAAATGGATCCTTTTGTACGATCA	1080	PR 29-OCT-1998;	98WO-US022992
Qy	1081	CTTATATCACTCTGTATATGACTAAGTAAACAAAAGTGAGAGTAATTTATTTGTAATGGA	1140	PR 20-NOV-1998;	98WO-US024855
Db	1081	CTTATATCACTCTGTATATGACTAAGTAAACAAAAGTGAGAGTAATTTATTTGTAATGGA	1140	PR 01-DEC-1998;	98WO-US025108
Qy	1141	TGGATAAAAATGGAATTTACTCATATACAGGGTGGAAATTTTATCTCTGTTATCACACCAACA	1200	PR 05-JAN-1999;	98WO-US000106
Db	1141	TGGATAAAAATGGAATTTACTCATATACAGGGTGGAAATTTTATCTCTGTTATCACACCAACA	1200	PR 08-MAR-1999;	98WO-US005028
Qy	1201	GTTCATATATATTTTCTGAATATCATCGCCCTTAATAGGACAATTTCTATTTGTTGACCAAT	1260	PR 10-MAR-1999;	98WO-US005190
Db	1201	GTTCATATATATTTTCTGAATATCATCGCCCTTAATAGGACAATTTCTATTTGTTGACCAAT	1260	PR 20-APR-1999;	98WO-US008615
Qy	1261	TCTACAAATTTGTAAAGTCCAATCTGTCTTAATTAAGTAATAATCATCTCTTTT	1320	PR 14-MAY-1999;	98WO-US010733
Db	1261	TCTACAAATTTGTAAAGTCCAATCTGTCTTAATTAAGTAATAATCATCTCTTTT	1320	PR 02-JUN-1999;	98WO-US012252
Qy	1321	AAAAAAAAAAAAAAAAAAAAAAAAAAAA 1346		PR 01-SEP-1999;	98WO-US020111
Db	1321	AAAAAAAAAAAAAAAAAAAAAAAAAAAA 1346		PR 08-SEP-1999;	98WO-US020594
RESULT 15					98WO-US020944
ABX89381					98WO-US021090
ID	ABX89381 standard; cDNA; 1346 BP.				98WO-US021547
XX					98WO-US023089
AC	ABX89381;				98WO-US028214
XX					98WO-US028313
DT	13-MAY-2003 (first entry)				98WO-US028409
DE	DNA encoding novel secreted and transmembrane protein PRO1312.				98WO-US028301
XX					98WO-US028364
KW	Human; PRO; hypertrophy of neonatal heart; angiogenesis; wound healing;				98WO-US028565
KW	cardiac insufficiency disorder; cancer; tumour; immune response;				98WO-US030095
KW	adrenal cortical capillary endothelial growth; c-fos induction;				98WO-US030911
KW	vascular endothelial growth factor inhibition; VEGF inhibition;				98WO-US030999
KW	endothelial cell growth inhibitor; T-lymphocytes stimulation;				98WO-US030720
KW	retinal neurons cell survival; rod photoreceptor cell survival;				98WO-US031243
KW	retinal disorder; retinitis pigmentosa; kidney disease;				98WO-US031274
KW	mammalian kidney mesangial cell proliferation; Berger disease;				2000WO-US000219
KW	dermatitis; herpeticiformis; Crohn's disease; chondrocyte proliferation;				2000WO-US000277
KW	chondrocyte redifferentiation; sports injury; arthritis; gene; ss.				2000WO-US000376
XX	Homo sapiens.				2000WO-US003565
OS	US2003017563-A1.				2000WO-US004341
XX	23-JAN-2003.				2000WO-US004342
XX					2000WO-US004414
XX					2000WO-US004914
XX					2000WO-US005004
XX					2000WO-US005601
XX					2000WO-US005746
XX					2000WO-US005841
XX					2000WO-US006319
XX					2000WO-US006884
XX					2000WO-US007377

PR 05-APR-2001; 2001US-00828366.
PR 10-MAY-2001; 2001US-00854208.
PR 10-MAY-2001; 2001US-00854280.
PR 18-MAY-2001; 2001US-00860216.
PR 25-MAY-2001; 2001US-00866028.
PR 25-MAY-2001; 2001US-00866034.
PR 25-MAY-2001; 2001WO-US017092.
PR 01-JUN-2001; 2001US-00872035.
PR 01-JUN-2001; 2001WO-US017800.
PR 05-JUN-2001; 2001US-00874503.
PR 14-JUN-2001; 2001US-00882636.
PR 19-JUN-2001; 2001US-00886342.
PR 20-JUN-2001; 2001WO-US019692.
PR 21-JUN-2001; 2001US-00887879.
PR 22-JUN-2001; 2001WO-US020116.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 18-JUL-2001; 2001US-00908827.
PR 06-AUG-2001; 2001US-00924419.
PR 09-AUG-2001; 2001US-00927796.
PR 16-AUG-2001; 2001US-00931836.
PR 19-DEC-2001; 2001US-00028072.

(GETH) GENENTECH INC.

PI Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;
PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
XX
DR WPI; 2003-148238/14.
DR P-PSDB; ABU59891.
XX
PT Two hundred and seventy five nucleic acids encoding PRO polypeptides,
PT useful for treating pericyte-associated tumors, diabetes and various bone
PT and/or cartilage disorders, e.g. arthritis.

PS Claim 2; Fig 481; 659pp; English.

XX The invention describes an isolated human PRO polypeptide. The PRO
CC polypeptides are useful in detecting PRO polypeptides in a sample, in
CC linking a bioactive molecule to a cell expressing a PRO polypeptide, and
CC in modulating at least one biological activity of a cell expressing a PRO
CC polypeptide. PRO1312 stimulates hypertrophy of neonatal heart and is thus
CC useful for treating cardiac insufficiency disorders. PRO1154 and PRO1186
CC stimulate adrenal cortical capillary endothelial growth, and PRO536,
CC PRO943, PRO828, PRO1068 or PRO535, PRO826, PRO819, PRO1126,
CC PRO1360 and PRO1387 induce c-fos in endothelial cells, and are thus
CC useful for treating conditions or disorders where angiogenesis would be
CC beneficial, e.g. wound healing and antagonist of this polypeptide are
CC useful for treating cancerous tumours. PRO812 inhibits vascular
CC endothelial growth factor (VEGF) stimulated proliferation of endothelial
CC cells and is thus useful for inhibiting endothelial cell growth in
CC mammals which would be beneficial in inhibiting tumour growth. PRO826,
CC PRO1068, PRO1184, PRO1346 and PRO1375 stimulate proliferation of
CC stimulated T-lymphocytes and are therapeutically useful for enhancing
CC immune response. PRO828, PRO826, PRO1068 or PRO1132 enhance survival of
CC retinal neurons cells (PRO1132 is also enhances survival/proliferation of
CC rod photoreceptor cells) and therefore are useful for treating retinal
CC disorders of injuries, e.g. retinitis pigmentosa, AMD. PRO819, PRO813
CC and PRO1066 induce proliferation of mammalian kidney mesangial cells,
CC and therefore are useful for treating kidney disorders associated with
CC decreased mesangial cell function such as Berger disease or other
CC nephropathies associated with dermatitis, herpeticiformis or Crohn's
CC disease. PRO1310, PRO844, PRO1312, PRO1192 and PRO1387 induce the
CC proliferation and/or redifferentiation of chondrocytes in culture and are
CC thus useful for treating sports injuries, and arthritis. This sequence
XX encodes a novel human PRO protein

SQ Sequence 1346 BP; 457 A; 245 C; 237 G; 407 T; 0 U; 0 Other;

Query Match 100.0%; Score 1346; DB 7; Length 1346;
Best Local Similarity 100.0%; Pred. No. 1.6e-262;
Matches 1346; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	GAAAGAATGTTGGCTGCTCTTTTCTGGTGACGCGCCATTTCATGCTGAACTCTGTCAA	60
Db	1	GAAAGAATGTTGGCTGCTCTTTTCTGGTGACGCGCCATTTCATGCTGAACTCTGTCAA	60
QY	61	CCAGGTGCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAAACAGCTCTGGGAGATAA	120
Db	61	CCAGGTGCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAAACAGCTCTGGGAGATAA	120
QY	121	GCATATGCTGGGATACCAATGAAGAAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATG	180
Db	121	GCATATGCTGGGATACCAATGAAGAAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATG	180
QY	181	AGAAAAGTTCCCAACAGAGAAGCAACAGAAAATTTCCCATGTCTTCTTCAATGTAACC	240
Db	181	AGAAAAGTTCCCAACAGAGAAGCAACAGAAAATTTCCCATGTCTTCTTCAATGTAACC	240
QY	241	CAGAGGGTATCAATCTGCTGTTTGGTTTACAGACCCCTTCAAAAAATCACACCCCTTCCCTGCT	300
Db	241	CAGAGGGTATCAATCTGCTGTTTGGTTTACAGACCCCTTCAAAAAATCACACCCCTTCCCTGCT	300
QY	301	GTTGAGGTGCAATCAGCCATTAAGAAATGAACAAAGAACCGGATCAACAAATGCTTCTTTCTA	360
Db	301	GTTGAGGTGCAATCAGCCATTAAGAAATGAACAAAGAACCGGATCAACAAATGCTTCTTTCTA	360
QY	361	AATGACCAAACTCTGGAATTTTAAAAATCCCTTCCACACTTGCACCCCATGGACCCA	420
Db	361	AATGACCAAACTCTGGAATTTTAAAAATCCCTTCCACACTTGCACCCCATGGACCCA	420
QY	421	TCTGTGCCCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATT	480
Db	421	TCTGTGCCCCATCTGGATTATTATTTGGTGTGATATTTTGCATCATCATAGTTGCAATT	480
QY	481	GCATCTACTGATTTTATCAGGGATCTGCAACGTTAGAGAAAGAACAAAGAACCATCTGAA	540
Db	481	GCATCTACTGATTTTATCAGGGATCTGCAACGTTAGAGAAAGAACAAAGAACCATCTGAA	540
QY	541	GTGGATGACGCTGAAGATAAGTGTGAAAAACATGATCACAATTTGAAAATGGCATCCCTCT	600
Db	541	GTGGATGACGCTGAAGATAAGTGTGAAAAACATGATCACAATTTGAAAATGGCATCCCTCT	600
QY	601	GATCCCTGGACATGAAGGGGGGCATATTAAATGATGCTTTCATGACAGAGGATGAGAGGC	660
Db	601	GATCCCTGGACATGAAGGGGGGCATATTAAATGATGCTTTCATGACAGAGGATGAGAGGC	660
QY	661	TCACCCCTCTCTGAAGGGCTGTTGTTCTGCTTCCCTCAAGAAATTAACATTTGTTCTGT	720
Db	661	TCACCCCTCTCTGAAGGGCTGTTGTTCTGCTTCCCTCAAGAAATTAACATTTGTTCTGT	720
QY	721	GTGACTGCTGACCATCTGAAATACCAAGAGCAGATCATATATTTGTTTTCACCATTTCTT	780
Db	721	GTGACTGCTGACCATCTGAAATACCAAGAGCAGATCATATATTTGTTTTCACCATTTCTT	780
QY	781	CTTTTGTAAATAAATTTTGAATGTCTTGAAGTGAAGAAAGCAATCAATTATACCCCAAC	840
Db	781	CTTTTGTAAATAAATTTTGAATGTCTTGAAGTGAAGAAAGCAATCAATTATACCCCAAC	840
QY	841	ACCACGAAATCATAGCTATTTCACGACTCAAAATATTCTAAATATTCTTCTGACAGTA	900
Db	841	ACCACGAAATCATAGCTATTTCACGACTCAAAATATTCTAAATATTCTTCTGACAGTA	900
QY	901	TAGTGATAAATGTGGTCATGTGGTATTGTAGTTATTGATTTAAGCAATTTTAGAATA	960
Db	901	TAGTGATAAATGTGGTCATGTGGTATTGTAGTTATTGATTTAAGCAATTTTAGAATA	960
QY	961	AGATCAGGCATATGTATATATTTTCACTTCAAGAGCTTAAGGAAAAAATAAATTTTCCA	1020
Db	961	AGATCAGGCATATGTATATATTTTCACTTCAAGAGCTTAAGGAAAAAATAAATTTTCCA	1020
QY	1021	GTGGAGAAATACATATATATGTTGTAGAAATCATTTGAAATGGATCCTTTTGGACGATCA	1080
Db	1021	GTGGAGAAATACATATATATGTTGTAGAAATCATTTGAAATGGATCCTTTTGGACGATCA	1080


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Qy 1081 CTTATATCACTCTGTATATGACTAAGTAAACAAAGTGAGAAGTAATTATTGTAAATGGA 1140
Db |||||
Qy 1081 CTTATATCACTCTGTATATGACTAAGTAAACAAAGTGAGAAGTAATTATTGTAAATGGA 1140
Db |||||
Qy 1141 TGGATAAAATGGAAATTTACTCATATACAGGGTGGAAATTTTATCCCTGTTATCACACCAACA 1200
Db |||||
Qy 1141 TGGATAAAATGGAAATTTACTCATATACAGGGTGGAAATTTTATCCCTGTTATCACACCAACA 1200
Db |||||
Qy 1201 GTTGATTATATATTTTCTGAATATCAGCCCTAATAGGACAATTTCTATTGTTGACCATT 1260
Db |||||
Qy 1201 GTTGATTATATATTTTCTGAATATCAGCCCTAATAGGACAATTTCTATTGTTGACCATT 1260
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Qy 1261 TCTACAATTTGTAAGTCCCAATCTGTGCTAACTTAATAAGTAATAATCATCTCTTTT 1320
Db |||||
Qy 1261 TCTACAATTTGTAAGTCCCAATCTGTGCTAACTTAATAAGTAATAATCATCTCTTTT 1320
Db |||||
Qy 1321 AAAAAAAAAAAAAAAAAAAAAA 1346
Db |||||
Qy 1321 AAAAAAAAAAAAAAAAAAAAAA 1346
Db |||||
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Search completed: April 3, 2004, 20:47:23
Job time : 663 secs

Result No.	Score	Query		DB	ID	Description
		Match	%			
1	845.2	62.8		3	US-09-289-349-6	Sequence 6, Appli
2	799.4	59.4		3	US-08-905-223-27	Sequence 27, Appl
3	799.4	59.4		4	US-09-247-155-27	Sequence 27, Appl
4	799.4	59.4		4	US-09-663-600A-27	Sequence 27, Appl
5	799.4	59.4		4	US-09-621-976-5	Sequence 5, Appli
6	125	9.3		3	US-08-989-299-3	Sequence 3, Appli
7	125	9.3		4	US-09-407-427-3	Sequence 3, Appli
8	125	9.3		3	US-08-989-299-1	Sequence 1, Appli
9	125	9.3		4	US-10-158-847-141	Sequence 141, App
10	125	9.3		4	US-09-407-427-1	Sequence 1, Appli
11	117	8.7		4	US-10-158-847-137	Sequence 137, App
12	69.4	5.2		4	US-09-280-116-40	Sequence 40, Appl
13	54	4.0		3	US-08-646-301A-1	Sequence 1, Appli
14	54	4.0		4	US-08-481-968A-4	Sequence 4, Appli
15	54	4.0		4	US-08-154-712B-4	Sequence 4, Appli
16	54	4.0		4	US-09-474-699-10	Sequence 10, Appl
17	52.8	3.9		4	US-09-843-376-10	Sequence 10, Appl
18	51.6	3.8		4	US-09-426-290-1	Sequence 1, Appli
19	47.8	3.6		3	US-08-998-416-1137	Sequence 1137, Ap
20	47.6	3.5		3	US-08-617-860B-28	Sequence 28, Appl
21	47.6	3.5		4	US-09-627-376-3	Sequence 3, Appli
22	47.2	3.5		4	US-10-204-708-22	Sequence 22, Appl
23	45.8	3.4		4	US-09-489-847-42	Sequence 42, Appl
24	45.6	3.4		4	US-09-540-236-28	GENERAL INFORMATI
25	45.4	3.4		3	US-08-998-416-186	Sequence 186, App
26	45.4	3.4		4	US-08-961-527-263	Sequence 263, App
27	44.8	3.3		3	US-08-998-416-288	Sequence 288, App

Db 301 CACCATCTCTTTTGTAAATAATTTGAATGTCTTGAAAGTGAAAGCAATCAATTAT 360
QY 831 ACCACCAACACCACTGAAATCATAAGCTATTCCAGACTCAAAATATTCTAAATATTTT 890
Db 361 ACCACCAACACCACTGAAATCATAAGCTATTCCAGACTCAAAATATTCTAAATATTTT 420
QY 891 TCTGACAGTATAGTGTATATAAATGTGCTCATGTGCTATTGTAGTTATTGATTAAGCAAT 950
Db 421 TCTGACAGTATAGTGTATATAAATGTGCTCATGTGCTATTGTAGTTATTGATTAAGCAAT 480
QY 951 TTTAGAAATAAGATCAGGCATATGTATATATTTTTCACACTTCAAGACCTTAAGGAAAAAT 1010
Db 481 TTTAGAAATAAGATCAGGCATATGTATATATTTTTCACACTTCAAGACCTTAAGGAAAAAT 540
QY 1011 AAATTTTCCAGTGGAGAAATACATATAATATGGGTAGAAATCAATTGAAATGGATCCTTT 1070
Db 541 AAATTTTCCAGTGGAGAAATACATATAATATGGGTAGAAATCAATTGAAATGGATCCTTT 600
QY 1071 TTGAGGATCACTTATATCACTCTGTATATGACTAAGTAAACAAAAGTGAGAAATAT 1130
Db 601 TTGAGGATCACTTATATCACTCTGTATATGACTAAGTAAACAAAAGTGAGAAATAT 660
QY 1131 TGTAAATGGATGGATAAATAATGGAATTAATCTATATACAGGGTGGAAATTTATCTCTGTTAT 1190
Db 661 TGTAAATGGATGGATAAATAATGGAATTAATCTATATACAGGGTGGAAATTTATCTCTGTTAT 720
QY 1191 CACACCAACAGTTGATTATATATTTTCTGAATATACAGCCCTTAATAGGACAAATCTATTT 1250
Db 721 CACACCAACAGTTGATTATATATTTTCTGAATATACAGCCCTTAATAGGACAAATCTATTT 780
QY 1251 GTTGACCATTTCTACAAATTTGTAAAGTCCAATCTGTGCTAACTTAATAAGTAATAATC 1310
Db 781 GTTGACCATTTCTACAAATTTGTAAAGTCCAATCTGTGCTAACTTAATAAGTAATAATC 840
QY 1311 ATCTCTTTTAAAAAATAAAAA 1332
Db 841 ATCTCTTAAAAAATAAAAAA 862

RESULT 2

US-08-905-223-27
; Sequence 27, Application US/08905223
; Patent No. 622029
; GENERAL INFORMATION:
; APPLICANT: Edwards, Jean-Baptiste D.
; APPLICANT: Duclert, Aymeric
; APPLICANT: Lacroix, Bruno
; TITLE OF INVENTION: 5' ESTs FOR SECRETED PROTEINS
; NUMBER OF SEQUENCES: 503
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson & Bear
; STREET: 501 West Broadway
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92101-3505
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Win95
; SOFTWARE: Word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/905,223
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Israelsen, Ned A.
; REGISTRATION NUMBER: 29,655
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 235-8550
; TELEFAX: (619) 235-0176
; INFORMATION FOR SEQ ID NO: 27:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 848 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: DOUBLE
; TOPOLOGY: LINEAR
; MOLECULE TYPE: CDNA
; ORIGINAL SOURCE:
; ORGANISM: Homo Sapiens
; DEVELOPMENTAL STAGE: Fetal
; TISSUE TYPE: kidney
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 32..73
; IDENTIFICATION METHOD: Von Heijne matrix
; OTHER INFORMATION: score 10.7
; OTHER INFORMATION: seq LWLLFLVTAIHA/EL
US-08-905-223-27
Query Match 59.4%; Score 799.4; DB 3; Length 848;
Best Local Similarity 98.8%; Pred. No. 7.2e-186;
Matches 809; Conservative 6; Mismatches 3; Indels 1; Gaps 1;
QY 1 GAAAGAAATGTTGTGCTGCTCTTTTCTGGTGAGCTGCCATTTCATGCTGAACTCTGTCAA 60
Db 26 GAAAGAAATGTTGTGCTGCTCTTTTCTGGTGAGCTGCCATTTCATGCTGAACTCTGTCAA 85
QY 61 CCAGGTGCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAA 120
Db 86 CCAGGTGCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAA 145
QY 121 GCATATGCTGGGATACCAATGAAGATACCTCTTCAAAGCGATGGTAGCTTTCTCCATG 180
Db 146 GCATATGCTGGGATACCAATGAAGATACCTCTTCAAAGCGATGGTAGCTTTCTCCATG 205
QY 181 AGAAAGATTCCCAACAGAGAGCAACAGAAAATTTCCCATGTCTTCTGCAATGTAAACC 240
Db 206 AGAAAGATTCCCAACAGAGAGCAACAGAAAATTTCCCATGTCTTCTGCAATGTAAACC 265
QY 241 CAGAGGGTATCATTTCTGGTTTGTGTTACAGACCTTCAAAAAATCACACCTTCTCTGCT 300
Db 266 CAGAGGGTATCATTTCTGGTTTGTGTTACAGACCTTCAAAAAATCACACCTTCTCTGCT 325
QY 301 GTTGAGGTGCAATCAGCCATAAGAAATGAACACCGGATCAACAATGCTTCTTTCTA 360
Db 326 GTTGAGGTGCAATCAGCCATAAGAAATGAACACCGGATCAACAATGCTTCTTTCTA 385
QY 361 AATGACCAAACTCTGGAATTTTAAAAATCCCTTCCACACTTGACCCACCATGGACCCA 420
Db 386 AATGACCAAACTCTGGAATTTTAAAAATCCCTTCCACACTTGACCCACCATGGACCCA 445
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Db 446 TCTGTGCCCATCTGGATTATATATTTTGGTGTGATATTTTGCATCATCATAGTTGCAATT 505
QY 481 GCCTACTGATTTTATCAGGGATCTGGCAACGTAGAGAAAGAACAAAGAACCATCTGAA 540
Db 506 GCCTACTGATTTTATCAGGGATCTGGCAACGTADAAARAAGAACAAAGAACCATCTGAA 565
QY 541 GTGGATGACGCTGAAGATAAGTGTGAAAAACATGATCACAATTTGAAAAATGGCATCCCTCT 600
Db 566 GTGGATGACGCTGAARATAAATGTGAAAAACATGATCACAATTTGAAAAATGGCATCCCTCT 625
QY 601 GATCCCTGGACATGAAGGG-GGGCATATTAATGATGCTTTCATGACAGAGGATGAGAGG 659
Db 626 GATCCCTGGACATGAAGGGGGGCATATTAATGATGCTTTCATGACAGAGGATGAGAGG 685
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Db 686 CTCACCCCTCTCTGAGGGCTGTGTTCTGTCTTCTCAARAATAAACAATTTGTTTCTG 745
QY 720 TGTGACTGCTGAGCATCTGAAATACCAAGAGCAGATCATATATTTTGTTCACCATTTCT 779
Db 746 TGTGACTGCTGAGCATCTGAAATACCAAGAGCAGATCATATATTTTGTTCACCATTTCT 805

QY 780 TCTTTTGTAAATAATTTTGAATGCTGCTTGAAGTGAATA 818
Db 806 TCTTTTGTAAATAATTTTGAATGCTGCTTGAAGTGAATA 844

RESULT 3
US-09-247-155-27
; Sequence 27, Application US/09247155A
; Patent No. 6312922
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, Jean-Baptiste
; APPLICANT: Duclert, Aymeric
; APPLICANT: Bougueleret, Lydie
; TITLE OF INVENTION: Complementary DNAs
; FILE REFERENCE: GENSET.021A
; CURRENT APPLICATION NUMBER: US/09/247,155A
; CURRENT FILING DATE: 1999-02-09
; EARLIER APPLICATION NUMBER: 60/074,121
; EARLIER FILING DATE: 1998-02-09
; EARLIER APPLICATION NUMBER: 60/081,563
; EARLIER FILING DATE: 1998-04-13
; EARLIER APPLICATION NUMBER: 60/096,116
; EARLIER FILING DATE: 1998-08-10
; EARLIER APPLICATION NUMBER: 60/099,273
; EARLIER FILING DATE: 1998-10-04
; NUMBER OF SEQ ID NOS: 182
; SOFTWARE: Patent.pm
; SEQ ID NO 27
; LENGTH: 848
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 32..73
; OTHER INFORMATION: Von Heijne matrix
US-09-247-155-27

Query Match 59.4%; Score 799.4; DB 4; Length 848;
Best Local Similarity 98.8%; Pred. No. 7.2e-186;
Matches 809; Conservative 6; Mismatches 3; Indels 1; Gaps 1;

QY 1 GAAAGAAATGTTGGCTGCTCTTTTCTGTTGAGTGCCTTCAATCATGCTGAACTCTGTCAA 60
Db 26 GAAAGAAATGTTGGCTGCTCTTTTCTGTTGAGTGCCTTCAATCATGCTGAACTCTGTCAA 85
QY 61 CCAGGTGCAGAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGAGATAAA 120
Db 86 CCAGGTGCAGAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGAGATAAA 145
QY 121 GCATATGCTGGGATACCAATGAAGTAACTCTTCAAGGCGATGGTAGCTTCTCCATG 180
Db 146 GCATATGCTGGGATACCAATGAAGTAACTCTTCAAGGCGATGGTAGCTTCTCCATG 205
QY 181 AGAAAGTTCCCAACAGAGAGCAACAGAAATTTCCCATGCTCTACTTTGCAATGTAACC 240
Db 206 AGAAAGTTCCCAACAGAGAGCAACAGAAATTTCCCATGCTCTACTTTGCAATGTAACC 265
QY 241 CAGAGGTATCATTTCTGTTTGTGTTTACAGCCCTTCAAAAAATCAGCCCTTCTGCT 300
Db 266 CAGAGGTATCATTTCTGTTTGTGTTTACAGCCCTTCAAAAAATCAGCCCTTCTGCT 325
QY 301 GTTGAGGTGCAATCAGCCATGAAGATGAACAGAACCGGATCAACAATGCTTCTTTCTA 360
Db 326 GTTGAGGTGCAATCAGCCATGAAGATGAACAGAACCGGATCAACAATGCTTCTTTCTA 385
QY 361 AATGACCAAACTCTGGAATTTTAAATCCCTTCCACACTTGCCACCACCATGGACCCA 420
Db 386 AATGACCAAACTCTGGAATTTTAAATCCCTTCCACACTTGCCACCACCATGGACCCA 445
QY 421 TCTGTGCCCATCTGGATTATATATTTTGGTGTGATATTTTGCATCATCATAGTTGCAATT 480
Db 446 TCTGTGCCCATCTGGATTATATATTTTGGTGTGATATTTTGCATCATCATAGTTGCAATT 505

QY 481 GCACTACTGATTTTATCAGGGATCTGGCAACGTTAGAGAAAGAACAAAGAACCATCTGAA 540
Db 506 GCACTACTGATTTTATCAGGGATCTGGCAACGTTAGAGAAAGAACAAAGAACCATCTGAA 565
QY 541 GTGGATGACGCTGAAGATAAGTGTGAAAAACATGATCACAATTTGAAAAATGGCATCCCTCT 600
Db 566 GTGGATGACGCTGAARATAAATGTGAAAAACATGATCACAATTTGAAAAATGGCATCCCTCT 625
QY 601 GATCCCTCTGGACATGAAGGG-GGGCATATTAATGATGCCTTCATGACAGAGGATGAGGG 659
Db 626 GATCCCTCTGGACATGAAGGGAGGAGCATATTAATGATGCCTTCATGACAGAGGATGAGGG 685
QY 660 CTCACCCCTCTCTGAAGGGCTGTTGTTCTGCTTCTCAAGAAATTAACATTTGTTCTG 719
Db 686 CTCACCCCTCTCTGAAGGGCTGTTGTTCTGCTTCTCAARAAATTAACATTTGTTCTG 745
QY 720 TGTGACTGCTGAGCATCTGAAATACCAAGAGAGAGATCATATATTTTGTTCACCATCT 779
Db 746 TGTGACTGCTGAGCATCTGAAATACCAAGAGAGAGATCATATATTTTGTTCACCATCT 805
QY 780 TCTTTTGTAAATAATTTTGAATGCTGCTTGAAGTGAATA 818
Db 806 TCTTTTGTAAATAATTTTGAATGCTGCTTGAAGTGAATA 844

RESULT 4
US-09-663-600A-27
; Sequence 27, Application US/09663600A
; Patent No. 6573068
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, Jean-Baptiste
; APPLICANT: Duclert, Aymeric
; APPLICANT: Bougueleret, Lydie
; TITLE OF INVENTION: EXTENDED CDNAS FOR SECRETED PROTEINS
; FILE REFERENCE: 31.US3.CIP
; CURRENT APPLICATION NUMBER: US/09/663,600A
; CURRENT FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: 09/191,997
; PRIOR FILING DATE: 1998-11-13
; PRIOR APPLICATION NUMBER: 60/066,677
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/069,957
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/074,121
; PRIOR FILING DATE: 1998-02-09
; PRIOR APPLICATION NUMBER: 60/081,563
; PRIOR FILING DATE: 1998-04-13
; PRIOR APPLICATION NUMBER: 60/096,116
; PRIOR FILING DATE: 1998-08-10
; PRIOR APPLICATION NUMBER: 60/099,273
; PRIOR FILING DATE: 1998-09-04
; NUMBER OF SEQ ID NOS: 229
; SOFTWARE: Patent.pm
; SEQ ID NO 27
; LENGTH: 848
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 32..73
; OTHER INFORMATION: Von Heijne matrix
US-09-663-600A-27

Query Match 59.4%; Score 799.4; DB 4; Length 848;
Best Local Similarity 98.8%; Pred. No. 7.2e-186;
Matches 809; Conservative 6; Mismatches 3; Indels 1; Gaps 1;
QY 1 GAAAGAAATGTTGGCTGCTCTTTTCTGTTGAGTGCCTTCAATCATGCTGAACTCTGTCAA 60
Db 26 GAAAGAAATGTTGGCTGCTCTTTTCTGTTGAGTGCCTTCAATCATGCTGAACTCTGTCAA 85
QY 61 CCAGGTGCAGAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGAGATAAA 120

Db 86 CCAGGTGCAGAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAA 145
Qy 121 GCATATGCTGGGATACCAATGAAGATACCTCTTCAAGCGATGGTAGCTTTCTCCATG 180
Db 146 GCATATGCTGGGATACCAATGAAGATACCTCTTCAAGCGATGGTAGCTTTCTCCATG 205
Qy 181 AGAAAGTTCCCAACAGAGAGCAACAGAAATTTCCCATGTCTCTACTTTGCAATGTAACC 240
Db 206 AGAAAGTTCCCAACAGAGAGCAACAGAAATTTCCCATGTCTCTACTTTGCAATGTAACC 265
Qy 241 CAGAGGGTATCATTTCTGGTTTGTGGTTACAGACCCCTTCAAAAAATCACACCTTCTCTGCT 300
Db 266 CAGAGGGTATCATTTCTGGTTTGTGGTTACAGACCCCTTCAAAAAATCACACCTTCTCTGCT 325
Qy 301 GTTGAGGTGCAATCAGCCATTAATATTTGGTGTGATATTTGTCATCATATGTCATTTCTTCTA 360
Db 326 GTTGAGGTGCAATCAGCCATTAATATTTGGTGTGATATTTGTCATCATATGTCATTTCTTCTA 385
Qy 361 AATGACCAAACTCTGGAAATTTTAAATCCCTTCCACACTTGGCACCACCCATGGACCCA 420
Db 386 AATGACCAAACTCTGGAAATTTTAAATCCCTTCCACACTTGGCACCACCCATGGACCCA 445
Qy 421 TCTGTGCCCATCTGGATTAATATTTGGTGTGATATTTGTCATCATATGTCATTTCTTCTA 480
Db 446 TCTGTGCCCATCTGGATTAATATTTGGTGTGATATTTGTCATCATATGTCATTTCTTCTA 505
Qy 481 GCATCTACTGATTTTATCAGGGATCTGGCAACGTAGAAACATGATCACAATTTGAAATGGCATCCCCTCT 600
Db 506 GCATCTACTGATTTTATCAGGGATCTGGCAACGTAGAAACATGATCACAATTTGAAATGGCATCCCCTCT 625
Qy 541 GTGGATGACGCTGAAGATAAGTGTGAAACATGATCACAATTTGAAATGGCATCCCCTCT 659
Db 566 GTGGATGACGCTGAAGATAAGTGTGAAACATGATCACAATTTGAAATGGCATCCCCTCT 685
Qy 601 GATCCCTCGGACATGAAGGG-GGGCATTAATATGTCGCTTCTCAAGAAATTAACATTTGTTCTG 719
Db 626 GATCCCTCGGACATGAAGGGGAGGCATTAATATGTCGCTTCTCAAGAAATTAACATTTGTTCTG 745
Qy 660 CTCACCCCTCTCTGAAGGGCTGTTGTTCTGCTTCTCAAGAAATTAACATTTGTTCTG 779
Db 746 TGTGACTGCTGAGCATCTCGAAATACCAAGAGCAGATCATATATTTGTTTCCACCATCT 805
Qy 780 TCTTTTGAATAAAATTTTGAATGTGCTTGAAGTGAATA 818
Db 806 TCTTTTGAATAAAATTTTGAATGTGCTTGAAGTGAATA 844

RESULT 5
US-09-621-976-5
; Sequence 5, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Robert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 5
; LENGTH: 848
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 32..697

; NAME/KEY: sig_peptide
; LOCATION: 32..73
; OTHER INFORMATION: Von Heijne matrix
US-09-621-976-5
Query Match 59.4%; Score 799.4; DB 4; Length 848;
Best local Similarity 98.8%; Pred. No. 7.2e-186;
Matches 809; Conservative 6; Mismatches 3; Indels 1; Gaps 1;
Qy 1 GAAGAATGTTGTGCTGCTCTTTTCTGGTGACCTGACCTCATCTGGAACCTCTGTCAA 60
Db 26 GAAGAATGTTGTGCTGCTCTTTTCTGGTGACCTGACCTCATCTGGAACCTCTGTCAA 85
Qy 61 CCAGGTGCAGAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAA 120
Db 86 CCAGGTGCAGAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAA 145
Qy 121 GCATATGCTGGGATACCAATGAAGATACCTCTTCAAGCGATGGTAGCTTTCTCCATG 180
Db 146 GCATATGCTGGGATACCAATGAAGATACCTCTTCAAGCGATGGTAGCTTTCTCCATG 205
Qy 181 AGAAAGTTCCCAACAGAGAGCAACAGAAATTTCCCATGTCTCTACTTTGCAANTGTAACC 240
Db 206 AGAAAGTTCCCAACAGAGAGCAACAGAAATTTCCCATGTCTCTACTTTGCAANTGTAACC 265
Qy 241 CAGAGGGTATCATTTCTGGTTTGTGGTTACAGACCCCTTCAAAAAATCACACCTTCTCTGCT 300
Db 266 CAGAGGGTATCATTTCTGGTTTGTGGTTACAGACCCCTTCAAAAAATCACACCTTCTCTGCT 325
Qy 301 GTTGAGGTGCAATCAGCCATTAAGAAATGAACAGAACCCGGATCAACAATGCTTTCTTCTA 360
Db 326 GTTGAGGTGCAATCAGCCATTAAGAAATGAACAGAACCCGGATCAACAATGCTTTCTTCTA 385
Qy 361 AATGACCAAACTCTGGAAATTTTAAATCCCTTCCACACTTGGCACCACCCATGGACCCA 420
Db 386 AATGACCAAACTCTGGAAATTTTAAATCCCTTCCACACTTGGCACCACCCATGGACCCA 445
Qy 421 TCTGTGCCCATCTGGATTAATATTTGGTGTGATATTTTGGTCATCATATGTCATTTGCAATT 480
Db 446 TCTGTGCCCATCTGGATTAATATTTGGTGTGATATTTTGGTCATCATATGTCATTTGCAATT 505
Qy 481 GCATCTACTGATTTTATCAGGGATCTGGCAACGTAGAAACATGATCACAATTTGAAATGGCATCCCCTCT 540
Db 506 GCATCTACTGATTTTATCAGGGATCTGGCAACGTAGAAACATGATCACAATTTGAAATGGCATCCCCTCT 565
Qy 541 GTGGATGACGCTGAAGATAAGTGTGAAACATGATCACAATTTGAAATGGCATCCCCTCT 600
Db 566 GTGGATGACGCTGAAGATAAGTGTGAAACATGATCACAATTTGAAATGGCATCCCCTCT 625
Qy 601 GATCCCTCGGACATGAAGGG-GGGCATTAATATGTCGCTTCTCAAGAAATTAACATTTGTTCTG 659
Db 626 GATCCCTCGGACATGAAGGGGAGGCATTAATATGTCGCTTCTCAAGAAATTAACATTTGTTCTG 685
Qy 660 CTCACCCCTCTCTGAAGGGCTGTTGTTCTGCTTCTCAAGAAATTAACATTTGTTCTG 719
Db 686 CTCACCCCTCTCTGAAGGGCTGTTGTTCTGCTTCTCAAGAAATTAACATTTGTTCTG 745
Qy 720 TGTGACTGCTGAGCATCTCGAAATACCAAGAGCAGATCATATATTTGTTTCCACCATCT 779
Db 746 TGTGACTGCTGAGCATCTCGAAATACCAAGAGCAGATCATATATTTGTTTCCACCATCT 805
Qy 780 TCTTTTGAATAAAATTTTGAATGTGCTTGAAGTGAATA 818
Db 806 TCTTTTGAATAAAATTTTGAATGTGCTTGAAGTGAATA 844

RESULT 6
US-08-989-299-3
; Sequence 3, Application US/08989299
; Patent No. 6194556
; GENERAL INFORMATION:
; APPLICANT: Acton, Susan L.
; APPLICANT: Robinson, Keith B.

; TITLE OF INVENTION: ANGIOTENSIN CONVERTING ENZYME HOMOLOG
; TITLE OF INVENTION: AND THERAPEUTIC AND DIAGNOSTIC USES THEREFOR
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY, HOAG & ELIOT LLP
; STREET: One Post Office Square
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109-2170
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/989,299
; FILING DATE: 11-DEC-1997
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Arnold E., Beth
; REGISTRATION NUMBER: 35,430
; REFERENCE/DOCKET NUMBER: MIA-025.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-832-1000
; TELEFAX: 617-832-7000
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2415 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-08-989-299-3

Query Match 9.3%; Score 125; DB 3; Length 2415;
Best Local Similarity 57.3%; Pred. No. 3.3e-21;
Matches 293; Conservative 0; Mismatches 200; Indels 18; Gaps 3;

Qy 54 CTGTCAACCCAGGTGCAGAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGG 113
Db 1827 CTGGAGTCCATATGCAGACCAAGCATCAAAGTGAGGATAGCCCTAAATCAGCTCTTGG 1886

Qy 114 AGATAAAGCATATGCTTGTGAGTACCAATGAAGATACCTCTTCAAAGCGATGGTAGCTTT 173
Db 1887 AGATAAAGCATATGAATGGAACGACAAATGAATGTACCTGTTCGATCATCTGTTGCATA 1946

Qy 174 CTCCATGAG--AAAGTTCACACAGAGAACCAAGCAAGAAATTTCCC-----A 218
Db 1947 TGCTATGAGCAGTACTTTTAAAGTAAATAATCAGATGATCTTTTGGGGAGGAGGA 2006

Qy 219 TGTCTACTTTGCAATGTAAACCCAGAGGGTATCATCTCTGTTTGTGGTTACAGACCTTC 278
Db 2007 TGTGCGAGTGGCTAATTTGAACCAAGAAATCTCCTTTAAATTTCTTGTCACTGCACCTAA 2066

Qy 279 AAAAAA---TCACACCTTCTCTGCTGTGAGGTGCAATCAGCCATAAGAAATGAACAAGAA 335
Db 2067 AAATGTGTCTGATATCATCTCTAGAACTGAAAGTGAAGAGGCCATCAGGATGTCCCGGAG 2126

Qy 336 CCGGATCAACAATGCTTCTTTCTAAATGACCAAACTCTGGAATTTTAAAAATCCCTTC 395
Db 2127 CCGTATCAATGATGCTTTCCGCTGTGAATGCAACAGCCCTAGAGTTTCTGGGATACAGCC 2186

Qy 396 CACACTTGCAACCAACCCATGAGCCCATCTGTCCTCATCTGGATTATATATTTGGTGTGAT 455
Db 2187 AACACTTGGACCTCCTAACCAAGCCCTGTTTCCATATGCTGATGTTTGTGGAGTTGT 2246

Qy 456 ATTTTGCATCATATGTTGCAATTCACACTACTGATTTTATCAGGGATCTGGCAACGTAG 515
Db 2247 GATGGGAGTGTAGTGGTGGCATTTGTCTATCTCTGATCTTCACTGGGATCAGAGATCGGAA 2306

Qy 516 AAGAAAGAACAAAGAACCACTCTGAAGTGGAT 546

Db 2307 GAAGAAAAATAAAGCAAGAGTGGAGAAAAAT 2337

RESULT 7
US-09-407-427-3
; Sequence 3, Application US/09407427
; Patent No. 6610497
; GENERAL INFORMATION:
; APPLICANT: Acton, Susan L.
; APPLICANT: Robison, Keith E.
; TITLE OF INVENTION: ANGIOTENSIN CONVERTING ENZYME HOMOLOG AND THERAPEUTIC
; TITLE OF INVENTION: AND DIAGNOSTIC USES THEREFOR
; FILE REFERENCE: MNI-132CP2
; CURRENT APPLICATION NUMBER: US/09/407,427
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 09/163,648
; PRIOR FILING DATE: 1998-09-30
; PRIOR APPLICATION NUMBER: 08/989,299
; PRIOR FILING DATE: 1997-12-11
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 3
; LENGTH: 2415
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-407-427-3

Query Match 9.3%; Score 125; DB 4; Length 2415;
Best Local Similarity 57.3%; Pred. No. 3.3e-21;
Matches 293; Conservative 0; Mismatches 200; Indels 18; Gaps 3;

Qy 54 CTGTCAACCCAGGTGCAGAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGG 113
Db 1827 CTGGAGTCCATATGCAGACCAAGCATCAAAGTGAGGATAGCCCTAAATCAGCTCTTGG 1886

Qy 114 AGATAAAGCATATGCTTGTGAGTACCAATGAAGATACCTCTTCAAAGCGATGGTAGCTTT 173
Db 1887 AGATAAAGCATATGAATGGAACGACAAATGAATGTACCTGTTCGATCATCTGTTGCATA 1946

Qy 174 CTCCATGAG--AAAGTTCACACAGAGAACCAAGCAAGAAATTTCCC-----A 218
Db 1947 TGCTATGAGCAGTACTTTTAAAGTAAATAATCAGATGATCTTTTGGGGAGGAGGA 2006

Qy 219 TGTCTACTTTGCAATGTAAACCCAGAGGGTATCATCTCTGTTTGTGGTTACAGACCTTC 278
Db 2007 TGTGCGAGTGGCTAATTTGAACCAAGAAATCTCCTTTAAATTTCTTGTCACTGCACCTAA 2066

Qy 279 AAAAAA---TCACACCTTCTCTGCTGTGAGGTGCAATCAGCCATAAGAAATGAACAAGAA 335
Db 2067 AAATGTGTCTGATATCATCTCTAGAACTGAAAGTGAAGAGGCCATCAGGATGTCCCGGAG 2126

Qy 336 CCGGATCAACAATGCTTCTTTCTAAATGACCAAACTCTGGAATTTTAAAAATCCCTTC 395
Db 2127 CCGTATCAATGATGCTTTCCGCTGTGAATGCAACAGCCCTAGAGTTTCTGGGATACAGCC 2186

Qy 396 CACACTTGCAACCAACCCATGAGCCCATCTGTCCTCATCTGGATTATATATTTGGTGTGAT 455
Db 2187 AACACTTGGACCTCCTAACCAAGCCCTGTTTCCATATGCTGATGTTTGTGGAGTTGT 2246

Qy 456 ATTTTGCATCATATGTTGCAATTCACACTACTGATTTTATCAGGGATCTGGCAACGTAG 515
Db 2247 GATGGGAGTGTAGTGGTGGCATTTGTCTATCTCTGATCTTCACTGGGATCAGAGATCGGAA 2306

Qy 516 AAGAAAGAACAAAGAACCACTCTGAAGTGGAT 546

Db 2307 GAAGAAAAATAAAGCAAGAGTGGAGAAAAAT 2337

RESULT 8
US-08-989-299-1
; Sequence 1, Application US/08989299
; Patent No. 6194556
; GENERAL INFORMATION:


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; GENERAL INFORMATION:
; APPLICANT: Acton, Susan L.
; APPLICANT: Robison, Keith E.
; TITLE OF INVENTION: ANGIOTENSIN CONVERTING ENZYME HOMOLOG AND THERAPEUTIC
; TITLE OF INVENTION: AND DIAGNOSTIC USES THEREFOR
; FILE REFERENCE: MNI-132CP2
; CURRENT APPLICATION NUMBER: US/09/407,427
; CURRENT FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 09/163,648
; PRIOR FILING DATE: 1998-09-30
; PRIOR APPLICATION NUMBER: 08/989,299
; PRIOR FILING DATE: 1997-12-11
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 3396
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (82)..(2496)
US-09-407-427-1

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	Query Match	9.3%;	Score 125;	DB 4;	Length 3396;
	Best Local Similarity	57.3%;	Pred. No. 3.7e-21;		
	Matches 293;	Conservative	0;	Mismatches 200;	Indels 18; Gaps 3;
QY	54	CTGTCAACCCAGTGCAGAAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGACTCTCGG	113		
Db	1908	CTGGAGTCCATATGCAGACCACAAAGCATCAAAGTGAGGATAAGCCTAAAATCAGCTCTTCG	1967		
QY	114	AGATAAAGCATATGCCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTT	173		
Db	1968	AGATAAAGCATATGAATGGAACGACAATGAATGTACCTGTTCCGATCATCTGTTGCATA	2027		
QY	174	CTCCATGAG--AAAAGTTCCEAACAGAGAAACAAAGAAATTCCC-----A	218		
Db	2028	TGCTATGAGGCAGTACTTTTAAAGTAATAAATCAGATGATCTCTTTTGGGGAGGAGGA	2087		
QY	219	TGTCCTACTTTTGC AATGTAACCCAGAGGGGTATCATTTCTGGTTGTGTTACAGACCCCTTC	278		
Db	2088	TGTGCGAGTGGCTAAITTTGAACCAAGAATCTCCTTTAATTTCTTTGTCACTGCACCTAA	2147		
QY	279	AAAAA---TCACACCCCTTCTGCTGTTGAGGTGCAATCAGCCATAAGAAATGAACAAGAA	335		
Db	2148	AAATGTGCTGATATCAITTCCTAGAACTGAAAGTTGAAAGGCCATCAGGATGTCCCGGAG	2207		
QY	336	CCGGATCAACAAATGCCTTCTTTCTAAATGACCAAACTCTGGAAATTTTTAAAAATCCCTTC	395		
Db	2208	CCGTATCAATGATGCTTTCOGTCTGAATGACAACAGCCTAGAGTTTCTGGGGATACAGCC	2267		
QY	396	CACACTTGCACCAOCCATGAGCCCATCTGTGCCCATCTGGATATTATATTGTTGGTGTGAT	455		
Db	2268	AACACTTGGACCTCCTACACAGCCCCCTGTTCCATAIGGCTGATTTGTTTTGGAGTTGT	2327		
QY	456	ATTTTGCATCATATAGTTGCCAATTGCCACTACTGATTTTATCAGGGATCTGGCAACGTAG	515		
Db	2328	GATGGAGTGATAGTGGTTGGCATTGTCTATCTCTGATCTTCACTGGGATCAGAGATCGGAA	2387		
QY	516	AAGAAAGAAACAAAGAACCATCTGAAGTGGAT	546		
Db	2388	GAAGAAATAATAAGCAAGAAAGTGGAGAAAT	2418		

RESULT 11
US-10-158-847-137
; Sequence 137, Application US/10158847
; Patent No. 6592865
; GENERAL INFORMATION:
; APPLICANT: Tom Parry et al.
; TITLE OF INVENTION: Method and Compositions for Modulating ACE-2 Activity
; FILE REFERENCE: PF557
; CURRENT APPLICATION NUMBER: US/10/158,847

```

; CURRENT FILING DATE: 2002-06-03
; PRIOR APPLICATION NUMBER: 60/295,004
; PRIOR FILING DATE: 2001-06-04
; NUMBER OF SEQ ID NOS: 158
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 137
; LENGTH: 2920
; TYPE: DNA
; ORGANISM: homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1707)..(1707)
; OTHER INFORMATION: n equals any amino acid
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (2702)..(2702)
; OTHER INFORMATION: n equals any amino acid
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (2749)..(2749)
; OTHER INFORMATION: n equals any amino acid
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (2757)..(2757)
; OTHER INFORMATION: n equals any amino acid
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (2788)..(2789)
; OTHER INFORMATION: n equals any amino acid
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (2819)..(2819)
; OTHER INFORMATION: n equals any amino acid
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (2835)..(2835)
; OTHER INFORMATION: n equals any amino acid
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (2856)..(2856)
; OTHER INFORMATION: n equals any amino acid
;
; US-10-158-847-137

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Query Match	8.7%	Score 117;	DB 4;	Length 2920;
Best Local Similarity	57.6%	Pred. No. 3.1e-19;		
Matches 276;	Conservative 0;	Mismatches 185;	Indels 18;	Gaps 3;
QY 54	CTGTCAAC	CAGGTG	CAGAAAAATG	CTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGG 113
DB				
1856	CTGGAGTCC	ATATGC	CAGACCAAG	CATCAAAAGTGAGGATAAGCTTAAATCAGCTCTGG 1915
QY 114	AGATAAAG	CATATG	CTGGGATAC	CAATGAAGAATACCTCTTCAAAAGCGATGGTAGCTTT 173
DB				
1916	AGATAAAG	CATATG	AAATGGAAC	GACAAATGAATGTACCTGTTCCGATCATCTGTTGCATA 1975
QY 174	CTCCATGAG	--AAAAG	TTCCCAAC	CAGAGAAGCAACAGAAAATTTCCC-----A 218
DB				
1976	TGCTATGAG	GCAGTACT	TTTTTAAAG	TAAAAAGTAAAAAATCAGATGATCTTTTGGGGAGGAGGA 2035
QY 219	TGTCTACT	TTTGCAAT	GTAAACC	CAGAGGGTATCATTTCTGGTTTGTGGTTACAGACCTTC 278
DB				
2036	TGTGCGAG	TGGCTAAT	TGAAACC	CAAGAATCTCCTTTAAATTTCTTTGTCACTGCACCTAA 2095
QY 279	AAAAAA--	--TCAC	ACCTTC	CTGCTGTGAGGTGCAATCAGCCCATAGAAATGAACAAGAA 335
DB				
2096	AAATGTGT	CTGATAT	CATCTCTA	GACTGAAGTTGAAAAGGCCCATCAGGATGTCCCGAG 2155
QY 336	CCGGATCA	ACAAATG	CTTTCT	TAATGACCAAACTCTCGAAATTTTAAAAATCCCTTC 395
DB				
2156	CCGTATCA	ATGATG	CTTCCGT	CTGTAATGACGACAGCCTAGAGTTTCTGGGGATACAGCC 2215
QY 396	CACACTTG	CACCA	CCCATGG	ACCCATCTGTGCCCATCTCGGATTATTATATTGGTGAT 455
DB				

Db 2216 AACATTGGACCTCCTAACACAGCCCCCTGTTTCCATATGGCTGATTGTTTGGAGTTGT 2275
Qy 456 ATTTTGCATCATATAGTTGCAATTGCACTACTGATTTTATCAGGGATCTGGCAACGTA 514
Db 2276 GATGGGAGTAGTGGTTGGCATTGTTCATCCTGATCTTCACTGGGATCAGAGATCGGA 2334

RESULT 12
US-09-280-116-40/c
; Sequence 40, Application US/09280116A
; Patent No. 6331427
; GENERAL INFORMATION:
; APPLICANT: Robison, Keith E.
; TITLE OF INVENTION: Nucleic Acid Molecules Encoding Human Protease Homologs
; FILE REFERENCE: 5800-24, 035800/176965
; CURRENT APPLICATION NUMBER: US/09/280,116A
; CURRENT FILING DATE: 1999-03-26
; NUMBER OF SEQ ID NOS: 268
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 40
; LENGTH: 2350
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: angiotensin-converting enzyme
US-09-280-116-40

Query Match 5.2%; Score 69.4; DB 4; Length 2350;
Best Local Similarity 55.1%; Pred. No. 1.2e-07;
Matches 211; Conservative 0; Mismatches 151; Indels 21; Gaps 3;
Qy 72 AAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAGCATATGCTG 131
Db 414 AAAGCATCAAAAGTGAGGATAAGCCCTAAATCAGCTCTTGGAGATAAGCATATGAATG 355
Qy 132 GGATACCAATGAAGTAATACCTCTTCAAGCGATGGTAGTTTCTCCATGAG--AAAAGTT 189
Db 354 GAACGACAAATGAATGTACCTGTTCGGATCATCTGTTGCATATGCTATGAGGCAGTACTT 295
Qy 190 CCCAACAGAGAAGCAACAGAAATTTCCC-----ATGTCCTACTTTGCAAT 234
Db 294 TTAAAGATAAAATAATCAGCATGATCTTTTGGGAGGAAGGATGTGCGAGTGGCTAAT 235
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; Sequence 1, Application US/08646301A
; Patent No. 6194211
; GENERAL INFORMATION:
; APPLICANT: Richards, Cynthia Ann
; APPLICANT: Huber, Brian E.
; TITLE OF INVENTION: Transcriptional Regulatory Sequence of Carcinoembryonic
; Patent No. 6194211
; TITLE OF INVENTION: Antigen for Expression Targeting
; FILE REFERENCE: PB1508USW
; CURRENT APPLICATION NUMBER: US/08/646,301A
; CURRENT FILING DATE: 1996-05-16

; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 11288
; TYPE: DNA
; ORGANISM: Homo sapiens
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Matches 118; Conservative 0; Mismatches 70; Indels 2; Gaps 2;
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; Patent No. 6300490
; GENERAL INFORMATION:
; APPLICANT: Huber, Brian
; APPLICANT: Richards, Cynthia
; TITLE OF INVENTION: Molecular Constructs Comprising a Carcinoembryonic Antigen (C
; TITLE OF INVENTION: Transcriptional Regulatory Region
; FILE REFERENCE: PB1087US4
; CURRENT APPLICATION NUMBER: US/08/481,968A
; CURRENT FILING DATE: 1998-06-07
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn version 3.0
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; LENGTH: 11288
; TYPE: DNA
; ORGANISM: Homo sapiens
US-08-481-968A-4

Query Match 4.0%; Score 54; DB 4; Length 11288;
Best Local Similarity 62.1%; Pred. No. 0.0011;
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
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2	1346	100.0	1346	9	US-09-989-723-386	Sequence 386, App
3	1346	100.0	1346	9	US-09-989-279-386	Sequence 386, App
4	1346	100.0	1346	9	US-09-989-727-386	Sequence 386, App
5	1346	100.0	1346	9	US-09-989-731-386	Sequence 386, App
6	1346	100.0	1346	9	US-09-989-732-386	Sequence 386, App
7	1346	100.0	1346	9	US-09-991-073-386	Sequence 386, App
8	1346	100.0	1346	9	US-09-990-442-386	Sequence 386, App
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ALIGNMENTS

RESULT 1

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; Sequence 386, Application US/09989722
; Patent No. US20020072067A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas P.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730PIC63
; CURRENT APPLICATION NUMBER: US/09/989,722
; CURRENT FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17

; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C62
; CURRENT APPLICATION NUMBER: US/09/989,723
; CURRENT FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
; PRIOR FILING DATE: 1997-11-12
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;; PRIOR FILING DATE: 1998-07-09

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; Sequence 386, Application US/09989279
; Patent No. US20020072496A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.

APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P27301C56
CURRENT APPLICATION NUMBER: US/09/989,279
CURRENT FILING DATE: 2001-11-19
PRIOR APPLICATION NUMBER: 60/049787
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; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 1346; DB 9; Length 1346;

Best Local Similarity 100.0%; Pred. No. 5.5e-289;

Matches 1346; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB	61	CCAGGTGCAGAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAA	120
QY	121	GCATATGCTGGGATACCAATGAAGATACCTCTTCAAGCGATGGTAGCTTTCTCCATG	180
DB	121	GCATATGCTGGGATACCAATGAAGATACCTCTTCAAGCGATGGTAGCTTTCTCCATG	180
QY	181	AGAAAAGTCCCAACAGAGAGCAAGCAAGAAATTTCCCATGTCTTCAATGTAACC	240
DB	181	AGAAAAGTCCCAACAGAGAGCAAGCAAGAAATTTCCCATGTCTTCAATGTAACC	240
QY	241	CAGAGGGTATCATCTGGTTTGGTTACAGACCTTCAAAAATCAGACCTTCCTGCT	300
DB	241	CAGAGGGTATCATCTGGTTTGGTTACAGACCTTCAAAAATCAGACCTTCCTGCT	300
QY	301	GTTGAGGTGCAATCAGCCCATAGAAATGAACAGACCGGATCAAAATGCTTCTTCTA	360
DB	301	GTTGAGGTGCAATCAGCCCATAGAAATGAACAGACCGGATCAAAATGCTTCTTCTA	360
QY	361	AATGACCAAACTCTGGAAATTTTAAATAATCCCTTCCACACTTGACCCACCGGACCCA	420
DB	361	AATGACCAAACTCTGGAAATTTTAAATAATCCCTTCCACACTTGACCCACCGGACCCA	420
QY	421	TCTGTGCCCATCTGGATTATTAATTTGGTGTGATTTTGGATCATCATAGTTCGAATT	480
DB	421	TCTGTGCCCATCTGGATTATTAATTTGGTGTGATTTTGGATCATCATAGTTCGAATT	480
QY	481	GCACTACTGATTTTATCAGGGATCTGGCAACGCTGAGAAAGAAAGAAACCAATCTGAA	540
DB			

Db	481	GCACTACTGATTTTATCAGGGATCTGGCAACGCTAGAAAGAAAGAAACCAATCTGAA	540
QY	541	GTGGATGACGCTGAAGATAAGTGTGAAACATGATCACAATTTGAAATGCGATCCCTCT	600
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QY	601	GATCCCTCTGACATGAAGGGGGCATATTAATGATGCTTCAAGAAATTAACATTTGTTCTGT	660
Db	601	GATCCCTCTGACATGAAGGGGGCATATTAATGATGCTTCAAGAAATTAACATTTGTTCTGT	660
QY	661	TCACCCCTCTCTGAAGGGCTGTTGTTCTGCTTCTTCAAGAAATTAACATTTGTTCTGT	720
Db	661	TCACCCCTCTCTGAAGGGCTGTTGTTCTGCTTCTTCAAGAAATTAACATTTGTTCTGT	720
QY	721	GTGACTGCTGAGCATCTGAAATACCAAGAGCAGATCATATATTTGTTTCCACCATCTT	780
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Db	841	ACCCTGAAATCATAGCTATTCACGACTCAAAATATTTTAAATAATTTTCTGACAGTA	900
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Db	1021	GTGAGAAATACATATAATATGTTAGTAAATCAATTTGATTTTAAAGCAATTTTAAATA	1080
QY	1081	CTTATATCACTCTGTATATGACTAAGTAAACAAAGTGAAGTAAATTTTAAATAATTA	1140
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QY	1141	TGGTAAATAATGGAATTAATCATATACAGGGTGAATTTTATCTGTTAFCACACCAACA	1200
Db	1141	TGGTAAATAATGGAATTAATCATATACAGGGTGAATTTTATCTGTTAFCACACCAACA	1200
QY	1201	GTTGATATATATTTTCTGAATATCAGCCCTTAATAGGACAAATTTCTATTTGACCAAT	1260
Db	1201	GTTGATATATATTTTCTGAATATCAGCCCTTAATAGGACAAATTTCTATTTGACCAAT	1260
QY	1261	TCTACAATTTGTTAAAGTCCCAATCTGTGCTAACTTAATAAGTAAATATATCTCTTTT	1320
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Db	1321	AAAAAAAAAAAAAAAAAAAAAAAAA 1346	

RESULT 4

US-09-989-727-386

; Sequence 386, Application US/09989727

; Patent No. US20020072497A1

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi J.

; APPLICANT: Baker, Kevin P.

; APPLICANT: Botstein, David

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; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730P1C65
; CURRENT APPLICATION NUMBER: US/09/989,727
; CURRENT FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
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Query Match	Score 1346;	DB 9;	Length 1346;
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Query Match 100.0%; Score 1346; DB 5;
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DB	61	CCAGGTGCAGAAATGCTTTTAAAGTGAGACTTAGTAT	120
QY	121	GCATATGCCCTGGGATACCAATGAAGAAATACCTCTT	180
DB	121	GCATATGCCCTGGGATACCAATGAAGAAATACCTCTT	180
QY	181	AGAAAAGTTCCTCAACAGAGAGCAACAGAAATTTCC	240
DB	181	AGAAAAGTTCCTCAACAGAGAGCAACAGAAATTTCC	240
QY	241	CAGAGGGTATCATTTCTGGTTTGTGTTACAGACCCTT	300
DB	241	CAGAGGGTATCATTTCTGGTTTGTGTTACAGACCCTT	300
QY	301	GTTGAGGTGCAATCAGCCATAAGAAATGAACAAGAAC	360
DB	301	GTTGAGGTGCAATCAGCCATAAGAAATGAACAAGAAC	360
QY	361	AATGACCAAACTCTGGAAATTTTAAAAATCCCTTCCAC	420

361	AAATGACCAAACTCTGGAAATTTTAAATAATCCCTTCCACACTTGCACCAACCCATGGACCCA	420
421	TCTGTGCCCATCTGGATTATATATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATT	480
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841	ACCACGTGAAATCATAGCTATTCAAGACTCAAAATATTTCTAAATATTTTCTGACAGTA	900
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901	TAGTGATAAAAATGTGGTCATGTGGTATTTGPGATTAATGATTTAAGCATTTTGTAGAAATA	960
901	TAGTGATAAAAATGTGGTCATGTGGTATTTGPGATTAATGATTTAAGCATTTTGTAGAAATA	960
961	AGATCAGGCATATGTATATATTTTCAACACTTCAAAAGACCTAAGGAAAAATAAAATTTTCCA	1020
961	AGATCAGGCATATGTATATATTTTCAACACTTCAAAAGACCTAAGGAAAAATAAAATTTTCCA	1020
1021	GTGGAGAAATACATATAATATGGTGTAGAAATCATTTGAAAAATGGATCCTTTTGTGACGATCA	1080
1021	GTGGAGAAATACATATAATATGGTGTAGAAATCATTTGAAAAATGGATCCTTTTGTGACGATCA	1080
1081	CTTATATCACTCTGTATATGACTAAAGTAAACAAAAAGTGAGAAATTAATTTGTAATGGA	1140
1081	CTTATATCACTCTGTATATGACTAAAGTAAACAAAAAGTGAGAAATTAATTTGTAATGGA	1140
1141	TGGATAAAAAATGGAATTAATCATATACAGGGTGGAAATTTTATCCTGTTATCACACCAACA	1200
1141	TGGATAAAAAATGGAATTAATCATATACAGGGTGGAAATTTTATCCTGTTATCACACCAACA	1200
1201	GTTGAATATATATTTTCTGAATATCAGCCCTTAATAGGACAAATTTCTATTTGTTGACCATT	1260
1201	GTTGAATATATATTTTCTGAATATCAGCCCTTAATAGGACAAATTTCTATTTGTTGACCATT	1260
1261	TCTACAATTTGTAAAGTCCAAATCTGTGCTTAATTAAGTAATTAATCATCTCTTTT	1320
1261	TCTACAATTTGTAAAGTCCAAATCTGTGCTTAATTAAGTAATTAATCATCTCTTTT	1320
1321	AAAAAAAAAAAAAAAAAAAAAAAAAAAA	1346
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RESULT 5
US-09-989-731-386
; Sequence 386. Application US/09989731
; Patent No. US20020103125A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.

APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730PLC70
CURRENT FILING DATE: 2001-11-20
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066770
PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/075945
PRIOR FILING DATE: 1998-02-25
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/083322
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PRIOR APPLICATION NUMBER: 60/087106
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PRIOR APPLICATION NUMBER: 60/090429
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090431
PRIOR FILING DATE: 1998-06-24

RESULT 6

US-09-989-732-386

; Sequence 386, Application US/09989732

; Patent No. US20020123463A1

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi J.

; APPLICANT: Baker, Kevin P.

; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

; APPLICANT: Eaton, Dan L.

; APPLICANT: Ferrara, Napoleone

; APPLICANT: Fong, Sherman

; APPLICANT: Gerber, Hanspeter

; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, J. Christopher

; APPLICANT: Gurney, Austin L.

; APPLICANT: Kljavin, Ivar J.

; APPLICANT: Napier, Mary A.

; APPLICANT: Pan, James

; APPLICANT: Paoni, Nicholas F.

; APPLICANT: Roy, Margaret Ann

; APPLICANT: Stewart, Timothy A.

; APPLICANT: Tumas, Daniel

; APPLICANT: Watanabe, Colin K.

; APPLICANT: Williams, P. Mickey

; APPLICANT: Wood, William I.

; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

; TITLE OF INVENTION: Acids Encoding the Same

; FILE REFERENCE: P2730P1C57

; CURRENT APPLICATION NUMBER: US/09/989,732

; CURRENT FILING DATE: 2001-11-19

; PRIOR APPLICATION NUMBER: 60/049787

; PRIOR FILING DATE: 1997-06-16

; PRIOR APPLICATION NUMBER: 60/062250

; PRIOR FILING DATE: 1997-10-17

; PRIOR APPLICATION NUMBER: 60/065186

; PRIOR FILING DATE: 1997-11-12

; PRIOR APPLICATION NUMBER: 60/065311

; PRIOR FILING DATE: 1997-11-13

; PRIOR APPLICATION NUMBER: 60/066770

; PRIOR FILING DATE: 1997-11-24

; PRIOR APPLICATION NUMBER: 60/075945

; PRIOR FILING DATE: 1998-02-25

; PRIOR APPLICATION NUMBER: 60/078910

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; PRIOR FILING DATE: 1998-04-28

; PRIOR APPLICATION NUMBER: 60/084600

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; PRIOR FILING DATE: 1998-06-02

; PRIOR APPLICATION NUMBER: 60/087827

; PRIOR FILING DATE: 1998-06-03

; PRIOR APPLICATION NUMBER: 60/088021

; PRIOR FILING DATE: 1998-06-04

; PRIOR APPLICATION NUMBER: 60/088025

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; PRIOR APPLICATION NUMBER: 60/090254
; PRIOR FILING DATE: 1998-06-22

Qy 1261 TCTACAAATTGTAAAGTCCAATCTGTGCTAACTTAATAAAGTAATAATCATCTCTTTT 1320
Db 1261 TCTACAAATTGTAAAGTCCAATCTGTGCTAACTTAATAAAGTAATAATCATCTCTTTT 1320
Qy 1321 AAAAAAAAAAAAAAAAAAAAAAAAAA 1346
Db 1321 AAAAAAAAAAAAAAAAAAAAAAAAAA 1346

RESULT 7

US-09-991-073-386
; Sequence 386, Application US/09991073
; Patent No. US20020127576A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730PLC15
; CURRENT APPLICATION NUMBER: US/09/991,073
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066770
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/075945
; PRIOR FILING DATE: 1998-02-25
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/083322
; PRIOR FILING DATE: 1998-04-28
; PRIOR APPLICATION NUMBER: 60/084600
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/087106
; PRIOR FILING DATE: 1998-05-28
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; PRIOR APPLICATION NUMBER: 60/087827
; PRIOR FILING DATE: 1998-06-03
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; PRIOR FILING DATE: 1998-06-04
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;; PRIOR APPLICATION NUMBER: 60/091982
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/092182
;; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 1346; DB 9; Length 1346;

Best Local Similarity 100.0%; Pred. No. 5.5e-289;

Matches 1346; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 121 GCATATGCCCTGGGATACCAATGAAGATACCTCTTCAAGCGATGGTAGCTTTCTCCATG 180
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Qy 181 AGAAAAGTTCCCAACAGAGAAGCAACAGAAAATTTCCCATGTCTTCTTCAATGTAACC 240
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; PRIOR FILING DATE: 1998-07-09
Query Match 100.0%; Score 1346; DB 9; Length 1346;
Best Local Similarity 100.0%; Pred. No. 5.5e-289;
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RESULT 9

US-09-991-163-386
; Sequence 386, Application US/09991163
; Patent No. US20020132253A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730P1C17
; CURRENT APPLICATION NUMBER: US/09/991.163
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/049787
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; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 1346; DB 9; Length 1346;
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Qy 1 GAAAGAAATGTTGGCTGCTCTTTTCTGGTGACTGCCATTCTGCTGAATCTGTCAA 60
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721 GTGACTGTGAGCATCTGAAATACCAAGAGCAGATCATATATTTTGTTCACCATTCIT 780
Qy 781 CTTTGTGTAATAATTTTGAATGCTTGAAGTAAGTAAGTAAGTAAGTAAGTAAGTAAGTA 840
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
781 CTTTGTGTAATAATTTTGAATGCTTGAAGTAAGTAAGTAAGTAAGTAAGTAAGTAAGTA 840
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; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 1346; DB 9; Length 1346;
Best Local Similarity 100.0%; Pred. No. 5.5e-289;
Matches 1346; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 GAAAGAAATGTTGTGGCTGCTCTTTTCTGGTGACTGCCAATCATGCTGAACTCTGTCAA 60

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Db 121 GCATATGCTGGGATACCAATGAAGATACCTCTTCAAGCGATGGTAGCTTTCTCCATG 180

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Db 181 AGAAAGTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCTTACATTTGCAATGTAACC 240

Qy 241 CAGAGGGTATCATTTCTGGTTTGTGGTTACAGACCCCTTCAAAAAATCACACCCCTTCTGCT 300
Db 241 CAGAGGGTATCATTTCTGGTTTGTGGTTACAGACCCCTTCAAAAAATCACACCCCTTCTGCT 300

Qy 301 GTTGAGGTGCAATCAGCCATGAAGATGAACAAAGAACCGGATCAACAATGCTTTCTTCTA 360
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Qy 361 AATGACCAAACTCTGGAATTTTAAAAATCCCTTCCACATTTGCACCACCCATGGACCCA 420
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RESULT 11
US-09-990-456-386
; Sequence 386, Application US/09990456
; Patent No. US20020137890A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same

; FILE REFERENCE: P2730P1C22
; CURRENT APPLICATION NUMBER: US/09/990,456
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
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; Sequence 386, Application US/09989721
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GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas P.
; APPLICANT: Roy, Margaret Ann

; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C55
; CURRENT APPLICATION NUMBER: US/09/989,721
; CURRENT FILING DATE: 2001-11-19
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Query Match 100.0%; Score 1346; DB 9; Length 1346;

Best Local Similarity 100.0%; Pred. No. 5.5e-289;

Matches 1346; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy	121	GCATATGCTGGGATACCAATGAAGTACCTCTTCAAGCGATGGTAGCTTCTCCATG	180
Db	121	GCATATGCTGGGATACCAATGAAGTACCTCTTCAAGCGATGGTAGCTTCTCCATG	180
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Qy	301	GTTGAGGTGCAATCAGCCATAAGAAATGAACAGAACCGGATCAACAATGCTTCTTTCTA	360
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Qy	481	GCACTACTGATTTTATCAGGGATCTGGCAACGTTAGAGAAAGAACAAAGAACCATCTGAA	540
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; Sequence 386, Application US/09992598
; Patent No. US20020160384A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
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; APPLICANT: Paoni, Nicholas F.
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; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
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Query Match 100.0%; Score 1346; DB 9; Length 1346;

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Db	121	GCATATGCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATG	180
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Db	181	AGAAAAGTTCCCAACAGAGAGAACAGAAATTTCCCATGTCTTCTGCAATGTAACC	240
Qy	241	CAGAGGGTATCATCTGTTTGTGTTACAGACCCCTTCAAAAAATCACACCCCTTCTGCT	300
Db	241	CAGAGGGTATCATCTGTTTGTGTTACAGACCCCTTCAAAAAATCACACCCCTTCTGCT	300
Qy	301	GTTGAGGTGCAATCAGCCCATAGAAATGAACAGACCGGATCAACAATGCCCTTCTTTCTA	360
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Qy	361	AATGACCAAACTCTGGAATTTTAAAAAATCCCTTCCACACATTGACACCCCATGGACCCA	420
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RESULT 14

US-09-989-293A-386
; Sequence 386, Application US/09989293A
; Patent No. US20020177164A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.

; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Baton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C66
; CURRENT APPLICATION NUMBER: US/09/989,293A
; CURRENT FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
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; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 1346; DB 9; Length 1346;

Best Local Similarity 100.0%; Pred. No. 5.5e-289;

Matches 1346; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 121 GCATATGCTGGGATACCAATGAAGAAATACCTTCTCAAAGCGATGGTAGCTTTCTCCATG 180

Db 121 GCATATGCTGGGATACCAATGAAGAAATACCTTCTCAAAGCGATGGTAGCTTTCTCCATG 180

QY 181 AGAAAAAGTTCCCAACAGAGAACCAAGAAATTTCCCATGTCTTCTCAATGTAACC 240

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RESULT 15
US-09-989-735-386
; Sequence 386, Application US/09989735
; Publication No. US20020193299A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas P.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730PIC61
; CURRENT APPLICATION NUMBER: US/09/989,735
; CURRENT FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066770
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/075945
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?	PRIOR FILING DATE: 1998-07-09	

Query Match 100.0%: Score 1346; DB 9; Length 1346;

Query Match	100.0%;	Score 1346;	DB 3;
Best Local Similarity	100.0%;	Pred. No. 5.5e-289;	

BEST LOCAL SIMILARITY 100.0%; PRED. NO. 3.3E-263;
Matches 1346; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	GAAAGAAATGTTGGCTGCTCTTTTTCTGGTGACTGCCAATTCATGCTGAACCTCTGTCAA	60
Dδ	1		
Qy	61	CCAGGTGCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACACAGCTCTGGGAGATAAA	120
Dδ	61		
Qy	121	GCATATGCCCTGGGATACCAATGAAGAATACTCTTCAAAGCGATGGTAGCTTTCTCCCATG	180
Dδ	121		

```
Qy 181 AGAAAAGTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCTCTACTTTGCAATGTAACC 240
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
181 AGAAAAGTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCTCTACTTTGCAATGTAACC 240
Qy 241 CAGAGGGTATCATTTCTGGTTTGTGGTTACAGACCCCTTCAAAAAATCACACCCCTTCTCTGCT 300
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
241 CAGAGGGTATCATTTCTGGTTTGTGGTTACAGACCCCTTCAAAAAATCACACCCCTTCTCTGCT 300
Qy 301 GTTGAGGTGCAATCAGCCATAAGAAATGAACAAGAACCGGATCAACAATGCCCTTCTTCTA 360
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
301 GTTGAGGTGCAATCAGCCATAAGAAATGAACAAGAACCGGATCAACAATGCCCTTCTTCTA 360
Qy 361 AATGACCAAACTCTGGAATTTTAAATAATCCCTTCCACACTTGCACCAACCCATGGACCCA 420
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
361 AATGACCAAACTCTGGAATTTTAAATAATCCCTTCCACACTTGCACCAACCCATGGACCCA 420
Qy 421 TCTGTGCCCATCTGGATTATTATTTTGGTGTGATATTTTGCATCATCATAGTTGCAATT 480
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
421 TCTGTGCCCATCTGGATTATTATTTTGGTGTGATATTTTGCATCATCATAGTTGCAATT 480
Qy 481 GCACTACTGATTTTATCAGGGATCTGGCAACGTAGAGAAAGAACAAAGAACCATCTGAA 540
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
481 GCACTACTGATTTTATCAGGGATCTGGCAACGTAGAGAAAGAACAAAGAACCATCTGAA 540
Qy 541 GTGGATGACGCTGAAGATAAGTGTGAAACATGATCACAATTGAATAATGGCATCCCTCT 600
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
541 GTGGATGACGCTGAAGATAAGTGTGAAACATGATCACAATTGAATAATGGCATCCCTCT 600
Qy 601 GATCCCTTGGACATGAAGGGGGGCATATTAAATGATGCCCTTATGACAGAGGATGAGAGGC 660
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
601 GATCCCTTGGACATGAAGGGGGGCATATTAAATGATGCCCTTATGACAGAGGATGAGAGGC 660
Qy 661 TCACCCCTCTCTGAAGGGCTGTGTTCTGCTTCTCCTCAAGAAATTAACATTTGTTTCTGT 720
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
661 TCACCCCTCTCTGAAGGGCTGTGTTCTGCTTCTCCTCAAGAAATTAACATTTGTTTCTGT 720
Qy 721 GTGACTGCTGAGCATCCTGAAATACCAAGAGCAGATCATATATTTTGTTCACCAATCTT 780
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
721 GTGACTGCTGAGCATCCTGAAATACCAAGAGCAGATCATATATTTTGTTCACCAATCTT 780
Qy 781 CTTTTGTAAATAATTTTGAATGTGCTTGAAAGTGAAAGCAATCAATATATACCCACCAAC 840
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
781 CTTTTGTAAATAATTTTGAATGTGCTTGAAAGTGAAAGCAATCAATATATACCCACCAAC 840
Qy 841 ACCACTGAAATCATAGCTATTACGACTCAAAATATTTCTAAATATTTTCTGACAGTA 900
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
841 ACCACTGAAATCATAGCTATTACGACTCAAAATATTTCTAAATATTTTCTGACAGTA 900
Qy 901 TAGTGATAAAATGTGGTCATGTGGTATTTGTAGTTATTGATTTAAGCATTTTGTAGAAATA 960
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
901 TAGTGATAAAATGTGGTCATGTGGTATTTGTAGTTATTGATTTAAGCATTTTGTAGAAATA 960
Qy 961 AGATCAGGCATATGTATATATTTTCACTTCAAGACCTAAGGAAATAATAATTTTCCA 1020
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
961 AGATCAGGCATATGTATATATTTTCACTTCAAGACCTAAGGAAATAATAATTTTCCA 1020
Qy 1021 GTGGAGATAACATATAATATGTTAGTAATCATTTGAAATGGATCCTTTTGTACGATCA 1080
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1021 GTGGAGATAACATATAATATGTTAGTAATCATTTGAAATGGATCCTTTTGTACGATCA 1080
Qy 1081 CTTATATCACTCTGTATATGACTAAGTAAACAAAAGTGAGAGTAAITATTGTAAATGGA 1140
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1081 CTTATATCACTCTGTATATGACTAAGTAAACAAAAGTGAGAGTAAITATTGTAAATGGA 1140
Qy 1141 TGGATAAAATGGAAITTACTCATATACAGGGTGGAAITTTTATCCTGTATCACACCAACA 1200
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1141 TGGATAAAATGGAAITTACTCATATACAGGGTGGAAITTTTATCCTGTATCACACCAACA 1200
Qy 1201 GTTGATTATATATTTTCTGAATATCAGCCCTAATAGGCAATTTCTATTGTTGACCAATT 1260
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1201 GTTGATTATATATTTTCTGAATATCAGCCCTAATAGGCAATTTCTATTGTTGACCAATT 1260
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Qy 1261 TCTACAATTTGTAAAAGTCCCAATCTGTGCTAACTTTAATAAGTAATAATCATCTCTTTTT 1320
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1261 TCTACAATTTGTAAAAGTCCCAATCTGTGCTAACTTTAATAAGTAATAATCATCTCTTTTT 1320
Qy 1321 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1346
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1321 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1346
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Search completed: April 4, 2004, 01:06:44
Job time : 596 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: April 3, 2004, 19:52:32 ; Search time 3956 Seconds
(without alignments)
10160.388 Million cell updates/sec

Title: US-09-989-724-386
Perfect score: 1346
Sequence: 1 gaaagaatgtgtgtgtgtct.....aaaaaaaaaaaaaaaaaaaa 1346

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_estc:*
9: gb_est1:*
10: gb_est2:*
11: gb_est3:*
12: gb_est4:*
13: gb_est5:*
14: gb_estfun:*
15: em_eston:*
16: em_gss_hum:*
17: em_gss_inv:*
18: em_gss_pln:*
19: em_gss_vit:*
20: em_gss_fun:*
21: em_gss_mam:*
22: em_gss_mus:*
23: em_gss_pro:*
24: em_gss_rod:*
25: em_gss_phg:*
26: em_gss_vrl:*
27: gb_gss1:*
28: gb_gss2:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	791.2	58.8	870	12 BI760941	BI760941 603043142
2	751.2	55.8	978	12 BI762437	BI762437 603048828
3	746.8	55.5	779	12 BG217185	BG217185 RST36886
4	743.6	55.2	782	13 BU689227	BU689227 UI-CF-FNO

5	736.6	54.7	826	12	BG194741	BG194741 RST13907
6	732	54.4	788	12	BG211841	BG211841 RST31414
7	729	54.2	801	12	BG218203	BG218203 RST37930
8	715.4	53.2	750	14	CA312017	CA312017 UI-CF-FNO
9	706.8	52.5	780	12	BG429174	BG429174 602498032
10	704.4	52.3	754	12	BG181765	BG181765 RST618 AC
11	695.2	51.6	792	12	BG400845	BG400845 602464068
12	675.4	50.2	791	12	BG400319	BG400319 602464526
13	665.8	49.5	1081	12	BM811234	BM811234 AGENCOURT
14	661.6	49.2	855	12	BG427247	BG427247 602494304
15	657	48.8	669	29	AY399636	AY399636 Homo sapi
16	649.4	48.2	866	12	BG429618	BG429618 602501304
17	648.2	48.2	804	12	BG429705	BG429705 602493709
18	641.2	47.6	792	12	BG209271	BG209271 RST28786
19	639.4	47.5	850	12	BG430955	BG430955 602500255
20	637	47.3	782	12	BG433974	BG433974 602497274
21	636.8	47.3	688	12	BG776793	BG776793 602663969
22	633	47.0	668	12	BG400436	BG400436 602464461
23	631.4	46.9	736	12	BG399402	BG399402 602441161
24	628.4	46.7	888	12	BG400513	BG400513 602464748
25	627.8	46.6	835	12	BG564304	BG564304 602590019
26	625.4	46.5	663	14	CB139945	CB139945 K-EST0193
27	615	45.7	639	14	CB137859	CB137859 K-EST0190
28	615	45.7	808	12	BG399473	BG399473 602441206
29	612.2	45.5	781	12	BG193796	BG193796 RST12932
30	611.6	45.4	859	12	BG427839	BG427839 602501524
31	594.4	44.2	677	12	BG427745	BG427745 602497114
32	583	43.3	607	14	CB125058	CB125058 K-EST0173
33	582.6	43.3	801	12	BG428217	BG428217 602498872
34	580.4	43.1	1210	11	AK002337	AK002337 Mus muscu
35	579.2	43.0	866	12	BG188580	BG188580 RST7605 A
36	569	42.3	678	12	BG429011	BG429011 602501924
37	568.8	42.3	584	9	AI792241	AI792241 ov04f11.y
38	565.2	42.0	735	9	AV653898	AV653898 AV653898
39	564	41.9	884	12	BG399975	BG399975 602442028
40	563.2	41.8	570	9	AI793025	AI793025 qz39c10.y
41	562	41.8	571	10	AW242855	AW242855 xm90g11.x
42	561.2	41.7	765	9	AV652853	AV652853 AV652853
43	555	41.2	602	12	BG432624	BG432624 602500789
44	548.8	40.8	669	29	AY399637	AY399637 Pan trogl
45	544	40.4	828	12	BG195252	BG195252 RST14433

ALIGNMENTS

RESULT 1
BI760941
LOCUS 603043142F1 NIH_MGC_116 Homo sapiens cDNA clone IMAGE:5183554 5',
DEFINITION mRNA sequence.
ACCESSION BI760941
VERSION BI760941.1 GI:15752519
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 870)
NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11458 row: c column: 11
High quality sequence stop: 844.

FEATURES
source

Location/Qualifiers
1. .870
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5183554"
/lab_host="DH10B"
/clone_lib="NIH_MGC_116"
/note="Organ: pooled colon, kidney, stomach; Vector:
pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA
source anonymous pool of 3 colons, age 26 yo male, 49 yo
female, 71 yo male colon; 46 yo male kidney, and pool of 2
stomachs, 62 yo male and 70 yo female. Library is
oligo-dT primed and directionally cloned (EcoRV site is
destroyed upon cloning). Average insert size 1.4 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code
023. Note: this is a NIH_MGC Library."

ORIGIN

Query Match 58.8%; Score 791.2; DB 12; Length 870;
Best Local Similarity 97.7%; Pred. No. 4.7e-105;
Matches 813; Conservative 0; Mismatches 18; Indels 1; Gaps 1;

QY 11 TGTGGCTGCTCTTTTCTGGTACTGCCATTCATGCTGTAATCTGTCAACAGGTGCAG 70
DB 12 TGTGGCTGCTCTTTTCTGGTACTGCCATTCATGCTGTAATCTGTCAACAGGTGCAG 71

QY 71 AAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATATGCCT 130
DB 72 AAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATATGCCT 131

QY 131 GGGATACCAATGAAGATACCTCTTCAAAGCGATGGTAGCTTCTCCATGAGAAAGTTC 190
DB 132 GGGATACCAATGAAGATACCTCTTCAAAGCGATGGTAGCTTCTCCATGAGAAAGTTC 191

QY 191 CCAACAGAGAGCAACAGAAATTTCCCATGCTCTACTTTGCAATGTAACCCAGAGGTAT 250
DB 192 CCAACAGAGAGCAACAGAAATTTCCCATGCTCTACTTTGCAATGTAACCCAGAGGTAT 251

QY 251 CATTCTGGTTTGTGGTTACAGACCCCTTCAAAAATCACACCTTCTCTGCTGTGAGGTGC 310
DB 252 CATTCTGGTTTGTGGTTACAGACCCCTTCAAAAATCACACCTTCTCTGCTGTGAGGTGC 311

QY 311 AATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCCTTCTTTCTAATGACCAAA 370
DB 312 AATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCCTTCTTTCTAATGACCAAA 371

QY 371 CTCTGGAATTTTAAAAATCCCTTCCACACTTGCACCCACCCATGGACCCCATCTGTGCCCA 430
DB 372 CTCTGGAATTTTAAAAATCCCTTCCACACTTGCACCCACCCATGGACCCCATCTGTGCCCA 431

QY 431 TCTGGATTATTATATTTGGTGTGATATTTTGGCATCATCATAGTTGCAATTGCACTACTGA 490
DB 432 TCTGGATTATTATATTTGGTGTGATATTTTGGCATCATCATAGTTGCAATTGCACTACTGA 491

QY 491 TTTTATCAGGATCTGGCAACGTAGAGAAAGAAACAAAGAACCATCTGAAGTGGATGACG 550
DB 492 TTTTATCAGGATCTGGCAACGTAGAGAAAGAAACAAAGAACCATCTGAAGTGGATGACG 551

QY 551 CTGAAGATAAGTGTGAAAACATGATCAAAATTGAAAATGGGATCCCTCTGATCCCTGG 610
DB 552 CTGAAGATAAGTGTGAAAACATGATCAAAATTGAAAATGGGATCCCTCTGATCCCTGG 611

QY 611 ACATGAAGGG-GGGCATATTATGATGCCCTTATGACAGAGGATGAGAGGCTCACCCCTC 669
DB 612 ACATGAAGGGAGGGCATATTATGATGCCCTTATGACAGAGGATGAGAGGCTCACCCCTC 671

QY 670 TCTGAAGGGCTGTGTTCTGCTTCTCAAGAAATTAAACATTTTCTGTGACTGCT 729
DB 672 TCTGAAGGGCTGTGTTCTGCTTCTCAAGAAATTAAACATTTTCTGTGACTGCT 731

QY 730 GAGCATCTGTAATACCAAGACAGATCATATATTTTGTTCACCATCTCTCTTTGTAA 789
DB 732 GAGCATCTGTAATACCAAGACAGATCATATATTTTGTTCACCATCTCTCTTTGTAA 791

QY 790 TAAATTTTGAATGTCTTGAAGTGAAGCAATCAATATATATACCCACCAACA 841
DB 792 TAAATTTTGAATGTCTTGAAGTGAAGCAATCAATATATATACCCACCAACA 843

RESULT 2
BI762437
LOCUS 603048828F1 NIH_MGC_116 Homo sapiens cDNA clone IMAGE:5189023 5',
DEFINITION mRNA sequence.
ACCESSION BI762437
VERSION BI762437.1 GI:15754015
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 978)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11472 row: g column: 08
High quality sequence stop: 826.

FEATURES
Location/Qualifiers
1. .978
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5189023"
/lab_host="DH10B"
/clone_lib="NIH_MGC_116"
/note="Organ: pooled colon, kidney, stomach; Vector:
pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA
source anonymous pool of 3 colons, age 26 yo male, 49 yo
female, 71 yo male colon; 46 yo male kidney, and pool of 2
stomachs, 62 yo male and 70 yo female. Library is
oligo-dT primed and directionally cloned (EcoRV site is
destroyed upon cloning). Average insert size 1.4 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code
023. Note: this is a NIH_MGC Library."

ORIGIN

Query Match 55.8%; Score 751.2; DB 12; Length 978;
Best Local Similarity 92.9%; Pred. No. 2.5e-99;
Matches 863; Conservative 0; Mismatches 53; Indels 13; Gaps 7;

QY 35 CTGCCATTCTGCTGAACCTCTGTCAACCCAGGTGCAGAAAATGCTTTTAAAGTGAGACTTA 94
DB 1 CTGCCATTCTGCTGAACCTCTGTCAACCCAGGTGCAGAAAATGCTTTTAAAGTGAGACTTA 60

QY 95 GTATCAGAACAGCTCTGGGAGATAAAGCATATGCTGGGATACCAATGAAGAAATACCTCT 154
DB 61 GTATCAGAACAGCTCTGGGAGATAAAGCATATGCTGGGATACCAATGAAGAAATACCTCT 120

QY 155 TCAAGCGGATGGTAGCTTTCTCCATGAGAAAAGTTCCCAACAGAGAAGCAACAGAAATTT 214
DB 121 TCAAGCGGATGGTAGCTTTCTCCATGAGAAAAGTTCCCAACAGAGAAGCAACAGAAATTT 180


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|||||
670 ATTCTAAATATTTTCTGACAGTATAGTGATATAAATGGTCAATGGTATTTGTAGTT 729
|||||
936 ATTGATTAAAGCATTTTATAGAAATAAGATCAGGCATATGTATATATTTTC 985
|||||
730 ATTGATTAAAGCATTTTAAATAAATAAGATCAGGCATATGTATATATTTTC 779
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RESULT 4
BU689227/c
LOCUS
DEFINITION
UI-CF-EC1-adw-i-18-0-UI.81 UI-CF-EC1 Homo sapiens cDNA clone
UI-CF-EC1-adw-i-18-0-UI 3', mRNA sequence.
BU689227
BU689227.1 GI:23546785
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 782)
REFERENCE
AUTHORS
TITLE
Normalizaton and subtraction: two approaches to facilitate gene
discovery
JOURNAL
Genome Res. 6 (9), 791-806 (1996)
MEDLINE
97044477
PUBMED
8889548
COMMENT
Contact: McCray, PB
McCray Lab
University of Iowa
2024 University of Iowa Med Labs, Iowa City, IA 52242, USA
Tel: 319 356 4866
Fax: 319 356 7171
Email: paul-mccray@uiowa.edu
Tissue Procurement: Dr. M. J. Welsh, University of Iowa
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com) or from Open Biosystems
(www.openbiosystems.com).
Seq primer: M13 FORWARD
POLYA=Yes.

FEATURES
Source
1..782
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-CF-EC1-adw-i-18-0-UI"
/tissue_type="Lung"
/dev_stage="Adult and Fetal"
/lab_host="DH10B (Life Technologies) (T1 phage resistant)"
/clone_lib="UI-CF-EC1"
/note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a
modified polylinker; Site_1: EcoR I; Site_2: Not I;
UI-CF-EC1 is a normalized cDNA library containing the
following tissue(s): Normal lung from adult and from fetal
day 64, day 87, week 19 and week 42. The library was
constructed according to Bonaldo, Lennon and Soares,
Genome Research, 6:791-806, 1996. First strand cDNA
synthesis was primed with an oligo-dT primer containing a
Not I site. Double stranded cDNA was ligated to an EcoR I
adaptor, digested with Not I, and cloned directionally
into pT7T3-Pac vector. The oligonucleotide used to prime
the synthesis of first-strand cDNA contains a library tag
sequence that is located between the Not I site and the
(dT)18 tail. The sequence tag for this library is
AAGTGCCTTAC.
TAG_TISSUE=Normal Lung Epithelial Cells Tissue nos 369-371
and 380-383
TAG_LIB=UI-CF-EC1
TAG_SEQ=AAGTGCCTTAC"

ORIGIN
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Query Match 55.2%; Score 743.6; DB 13; Length 782;
Best Local Similarity 98.6%; Pred. No. 3.7e-98;
Matches 749; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 585 AAATGGCATCCCTCTGATCCCTCGACATGAAGGGGGGCATATTAATGATGCCTTCATG 644
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DB 760 AAAATGCATCCCTCTGATCCCTCGACATGAAGGGGGGCATATTAATGATGCCTTCATG 701

QY 645 ACAGAGGATGAGAGGCTCACCCCTCTCTGAAGGGCTGTGTTCTGCTTCTCAAGAAATT 704
|||
DB 700 ACAGAGGATGAGAGGCTCACCCCTCTCTGAAGGGCTGTGTTCTGCTTCTCAAGAAATT 641

QY 705 AAACATTTGTTCTGTGTGACTGCTGAGCATCCTGGAATACCAAGAGCAGATCATATATT 764
|||
DB 640 AAACATTTGTTCTGTGTGACTGCTGAGCATCCTGGAATACCAAGAGCAGATCATATATT 581

QY 765 TTGTTTCACCATTTCTTTTGTATAAATTTTGAATGTGCTTGAAGTGAAGCAATC 824
|||
DB 580 TTGTTTCACCATTTCTTTTGTATAAATTTTGAATGTGCTTGAAGTGAAGCAATC 521

QY 825 AATTATACCCACCAACACTGGAATCATAGCTATTTCAGCACTCAAAATATTCTAAAA 884
|||
DB 520 AATTATACCCACCAACACTGGAATCATAGCTATTTCAGCACTCAAAATATTCTAAAA 461

QY 885 TATTTTCTGACAGTATAGTGTATAAATGTGTCATGTGGTATTGTTAGTTATTTTA 944
|||
DB 460 TATTTTCTGACAGTATAGTGTATAAATGTGTCATGTGGTATTGTTAGTTATTTTA 401

QY 945 AGCATTTTGTAGAAATAAGATCAGGCATATGTATATATTTTCACACTTCAAGACCTAAGG 1004
|||
DB 400 AGCATTTTGTAGAAATAAGATCAGGCATATGTATATATTTTCACACTTCAAGACCTAAGG 341

QY 1005 AAAAATAAATTTTCCAGTGGAGATACATATAATATGGTGTAGAAATCATTTGAAAATGGA 1064
|||
DB 340 AAAAATAAATTTTCCAGTGGAGATACATATAATATGGTGTAGAAATCATTTGAAAATGGA 281

QY 1065 TCCTTTTGGACGATCACTTATATCTCTGTATATGACTAAGTAAACAAAAGTGAGAAGT 1124
|||
DB 280 TCCTTTTGGACGATCACTTATATCTCTGTATATGACTAAGTAAACAAAAGTGAGAAGT 221

QY 1125 AATTATTGTAATGGATGGATAAAATGGAATTACTCATATACAGGGTGGAAATTTTATCC 1184
|||
DB 220 AATTATTGTAATGGATGGATAAAATGGAATTACTCATATACAGGGTGGAAATTTTATCC 161

QY 1185 TGTATACACCAACAGTTGATTATATATATTTTCTGAATATCAGCCCTTAATAGGACAATT 1244
|||
DB 160 TGTATACACCAACAGTTGATTATATATATTTTCTGAATATCAGCCCTTAATAGGACAATT 101

QY 1245 CTATTTGTTGACCAATTTCTACAATTTGTAAAAGTCCAATCTGTGCTAACTTAATAAGTA 1304
|||
DB 100 CTATTTGTTGACCAATTTCTACAATTTGTAAAAGTCCAATTTGTGCTAACTTAATAAGTA 41

QY 1305 ATAATCATCTCTTTTAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 1344
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DB 40 ATAATCATCTCTTTTAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 1

RESULT 5
BG194741
LOCUS
DEFINITION
RST13907 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.
ACCESSION
BG194741
VERSION
BG194741.1 GI:13716428
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 826)
REFERENCE
AUTHORS
Harrington,J.J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R.,
Cain,S., Leventhal,C., Thornton,M., Ramachandran,R.,
Whittington,J., Lerner,L., Costanzo,D., McElligott,K., Booser,S.,
```

Mays,R., Smith,E., Veloso,N., Klika,A., Hess,J., Cothren,K., Lo,K.,
Offenbacher,J., Danzig,J. and Ducar,M.
Creation of genome-wide protein expression libraries using random
activation of gene expression

TITLE

JOURNAL
MEDLINE
PUBMED
COMMENT

Nat. Biotechnol. 19 (5), 440-445 (2001)
21227151
11329013
Contact: Scott J. Cain
Athersys, Inc.
3201 Carnegie Ave, Cleveland, OH 44115, USA
Tel: 216 431 9900
Fax: 216 361 9596
Email: scain@atersys.com
High quality sequence stop: 541.

FEATURES

source

1. .826
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/cell_line="HT1080"
/clone_lib="Athersys RAGE Library"
/note="See 'Creation of Genome-wide Protein Expression
Libraries using Random Activation of Gene Expression',
Nature Biotechnology, in press. Note that even though the
cell type indicated is HT1080, since a random activation
method was used, these sequence tags are not necessarily
expressed in HT1080 under normal circumstances."

ORIGIN

Query Match 54.7%; Score 736.6; DB 12; Length 826;
Best Local Similarity 96.7%; Pred. No. 3.6e-97;
Matches 792; Conservative 0; Mismatches 23; Indels 4; Gaps 4;

Qy 324 AATGAACAAGACCGGATCAACATGCCCTTCTTCTAAATGACCAAACTCTGGATTTT 383
Db 8 AATAGNACAANACCGGNTCAACATGCCCTTCTTCTAAATGACCAAACTCTGG-ATTTT 66
Qy 384 AAAATCCCTTCCACACTTGCACACCCCATGGACCCATCTGTGCCCATCTGGATTATTAT 443
Db 67 AAAATCCCTTCCACACTTGCACACCCCATGGACCCATCTGTGCCCATCTGGATTATTAT 126
Qy 444 ATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTCACACTACTGATTTTATCAGGGAT 503
Db 127 ATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTCACACTACTGATTTTATCAGGGAT 186
Qy 504 CTGGCAACGTAGAGAAAGAACCAAGAACCATCTGAAGTGGATGACGCTGAAGATAAGTG 563
Db 187 CTGGCAACGTAGAGAAAGAACCAAGAACCATCTGAAGTGGATGACGCTGAAGATAAGTG 246
Qy 564 TGAACAACATGATCACAATTGAATGGCATCCCTCTGATCCCTGGACATGAAGGG-GG 622
Db 247 TGAACAACATGATCACAATTGAATGGCATCCCTCTGATCCCTGGACATGAAGGGAGG 306
Qy 623 GCATATTAATGATGCCCTTCATGACAGAGGATGAGAGGCTCACCCCTCTCTGAAGGGCTGT 682
Db 307 GCATATTAATGATGCCCTTCATGACAGAGGATGAGAGGCTCACCCCTCTCTGAAGGGCTGT 366
Qy 683 TGTCTGCTTCTCAAGAAATTAACATTTGTTCTGTGACTGCTGAGCATCCTGAAA 742
Db 367 TGTCTGCTTCTCAAGAAATTAACATTTGTTCTGTGACTGCTGAGCATCCTGAAA 426
Qy 743 TACCAAGAGCAGATCATATATTTTGTTCACCATCTCTTTTGTAAATAAATTTGAATG 802
Db 427 TACCAAGAGCAGATCATATATTTTGTTCACCATCTCTTTTGTAAATAAATTTGAATG 486
Qy 803 TGCTTGAAAGTGAAAGCAATCAATATATACCCCAACACCATGAAATCATAAGCTATT 862
Db 487 TGCTTGAAAGTGAAAGCAATCAATATATACCCCAACACCATGAAATCATAAGCTATT 546
Qy 863 CAGGACTCAAAATATTTCTAAATATATTTTCTGACAGTATAGTGTATATAATGTGGTCAATG 922
Db 547 CAGGACTCANAAATATTTCTAAATATATTTTCTGACAGTATAGTGTATATAATGTGGTCAATG 606

Qy 923 GGTATTGTAGTTATTGATTTAAGCAATTTTAGAAATAAGATCAGGCATATGTATATA-T 981
Db 607 GGTATTGTAGTTATTGATTTAAGCAATTTTAGAAATAAGATCAGGCATATGTATATA-T 666
Qy 982 TTTTCACACTTCAAAGACCTAAGGAAATAAATTTTCCAGTGGAGAAATACATATAATAT- 1040
Db 667 TTTTCACACTTCAAAGACCTAAGGAAATAAATTTTCCAGTGGAGAAATACATATAATATG 726
Qy 1041 GGTGTAGAAATCATTTGAAATGGATCCTTTTTCAGCATCACTTATATCACTCTGTATATG 1100
Db 727 GGTGGAGAAATCATTTGAGAAAGGATCCTTTTGGCGATCACTTATATCACTCTGTATATG 786
Qy 1101 ACTAAGTAAACAAAAGTGAAGTAATATTATTGTAATGG 1139
Db 787 AACTAAGAAACACAAAGTGGGAAGTAATATTATTGTAGATGG 825

RESULT 6

BG211841

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

COMMENT

BG211841 788 bp mRNA linear EST 21-APR-2001
RST31414 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.
BG211841
BG211841.1 GI:13733528
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 788)
Harrington,J.J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R.,
Cain,S., Leventhal,C., Thornton,M., Ramachandran,R.,
Whittington,J., Lerner,L., Costanzo,D., McElligott,K., Booser,S.,
Mays,R., Smith,E., Veloso,N., Klika,A., Hess,J., Cothren,K., Lo,K.,
Offenbacher,J., Danzig,J. and Ducar,M.
Creation of genome-wide protein expression libraries using random
activation of gene expression
Nat. Biotechnol. 19 (5), 440-445 (2001)

FEATURES

source

1. .788
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/cell_line="HT1080"
/clone_lib="Athersys RAGE Library"
/note="See 'Creation of Genome-wide Protein Expression
Libraries using Random Activation of Gene Expression',
Nature Biotechnology, in press. Note that even though the
cell type indicated is HT1080, since a random activation
method was used, these sequence tags are not necessarily
expressed in HT1080 under normal circumstances."

ORIGIN

Query Match 54.4%; Score 732; DB 12; Length 788;
Best Local Similarity 98.2%; Pred. No. 1.7e-96;
Matches 771; Conservative 0; Mismatches 11; Indels 3; Gaps 3;

Qy 210 AATTTCCCATGTCCTACTTTTGCAATGTAAACCCAGAGGGTATCATTCGGTTTGTGTTAC 269
Db 6 AATTTACCATGTCCTACTTTTGTCATGTAAACCCAGAGGGTATCATTCGGTTTGTGTTAC 65
Qy 270 AGACCCCTTCAAAAATCACCCTTCTGCTGTGAGGTGCAATCAGCCATAAGAA 329
Db 66 AGACCCCTTCAAAAATCACCCTTCTGCTGTGAGGTGCAATCAGCCATAAGAA 125

QY 330 CAAGAACCGGATCAACAATGCCTTCTTTCTAAATGACCAAACTCTGGAATTTTAAAAAT 389
|||||
Db 126 CAAGAACCGGATCAACAATGCCTTCTTTCTAAATGA-CAAACTCTGGAATTTTAAAAAT 184
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QY 390 CCCTTCCACACTTGCACACCCATGACCCCATCTGTGCCCATCTGATGATTTATTTGG 449
|||||
Db 185 CCCTTCCACACTTGCACACCCATGACCCCATCTGTGCCCATCTGATGATTTATTTGG 244
|||||
QY 450 TGTGATATTTTGGATCATATAGTTGCAATGCACTACTGATTTTATCAGGGATCTGGCA 509
|||||
Db 245 TGTGATATTTTGGATCATATAGTTGTAATGCACTACTGATTTTATCAGGGATCTGGCA 304
|||||
QY 510 ACGTAGAAGAAAGAAACAAAGAACCACTCTGAAGTGGATGACGCTGAAGATAAGTGAATA 569
|||||
Db 305 ACGTAGAAGAAAGAAACAAAGAACCACTCTGAAGTGGATGACGCTGAAGATAAGTGAATA 364
|||||
QY 570 CATGATCACAATTTGAAATGGCATCCCTCTGATCCCTGGACATGAAGGG-GGGATAT 628
|||||
Db 365 CATGATCACAATTTGAAATGGCATCCCTCTGATCCCTGGACATGAAGGGGAGGCATAT 424
|||||
QY 629 TAATGATGCTTTCATGACAGAGGATGAGAGGCTACCCCTCTCTGAGGGCTGTGTTCT 688
|||||
Db 425 TAATGATGCTTTCATGACAGAGGATGAGAGGCTACCCCTCTCTGAGGGCTGTGTTCT 484
|||||
QY 689 GCTTCTCAAGAAATTAACAATTTGTTCTGTGTGACTGCTGAGCATCCTGAAATACCAA 748
|||||
Db 485 GCTTCTCAAGAAATTAACAATTTGTTCTGTGTGACTGCTGAGCATCCTGAAATACCAA 544
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QY 749 GAGCAGATCATATATTTGTTTCAACCATCTCTTTTGTGTAATAAATTTTGAATGCTTG 808
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Db 545 GAGCAGATCATATATTTGTTTCAACCATCTCTTTTGTGTAATAAATTTTGAATGCTTG 604
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QY 809 AAAGTGAAAGCAATCAATTAATACCCACCAACACCACTGAAATCAAGCTATTACAGAC 868
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Db 605 AAAGTGAAAGCAATCAATTAATACCCACCAACACCACTGAAATCAAGCTATTACAGAC 664
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QY 869 TCAAAATATTCTAAATATTTTCTGACAGTATAGTGTATAAATGTTGGTCATGTTGATT 928
|||||
Db 665 TCAAAATATTCTAAATATTTTCTGACAGTATAGTGTATAAATGTTGGTCATGTTGATT 724
|||||
QY 929 TGTAGTTATGATTTAAGCAATTTTGTAGAAATAAGATCAGGCATATGATATATTTTCA 988
|||||
Db 725 TGTAGTTATGATTTAAGCAATTTTGTAG- AATATGATCAAGCCTATGATATATTTTCA 783
|||||
QY 989 CTTCA 993
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Db 784 CTTA 788

RESULT 7
BG218203
LOCUS BG218203 801 bp mRNA linear EST 21-APR-2001
DEFINITION RST37930 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.
ACCESSION BG218203
VERSION BG218203.1 GI:13744224
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 801)
AUTHORS Harrington, J.J., Sherf, B., Rundlett, S., Jackson, P.D., Perry, R.,
Cain, S., Leventhal, C., Thornton, M., Ramachandran, R.,
Whittington, J., Lerner, L., Costanzo, D., McElligott, K., Boozer, S.,
Mays, R., Smith, E., Veloso, N., Klika, A., Hess, J., Cothren, K., Lo, K.,
Offenbacher, J., Danzig, J. and Ducar, M.
TITLE Creation of genome-wide protein expression libraries using random
activation of gene expression
JOURNAL Nat. Biotechnol. 19 (5), 440-445 (2001)
MEDLINE 21227151
PUBMED 11329013
COMMENT Contact: Scott J. Cain
Athersys, Inc.

3201 Carnegie Ave, Cleveland, OH 44115, USA
Tel: 216 431 9900
Fax: 216 361 9596
Email: scain@athersys.com
High quality sequence stop: 534.
Location/Qualifiers
1. 801
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/cell_line="HT1080"
/clone_lib="Athersys RAGE Library"
/note="See 'Creation of Genome-wide Protein Expression
Libraries using Random Activation of Gene Expression',
Nature Biotechnology, in press. Note that even though the
cell type indicated is HT1080, since a random activation
method was used, these sequence tags are not necessarily
expressed in HT1080 under normal circumstances."

ORIGIN

Query Match 54.2%; Score 729; DB 12; Length 801;
Best Local Similarity 96.4%; Pred. No. 4.6e-96;
Matches 767; Conservative 0; Mismatches 26; Indels 3; Gaps 2;
QY 213 TTCCCATGTCCTACTTTGCAATGTAACCCAGAGGGTATCATCTCTGTTTGTGTACAGA 272
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Db 5 TTTCCATGTCCTACTTTGCAATGTAACCCAGAGGGTATCATCTCTGTTTGTGTACAGA 64
|||
QY 273 CCCTTCAAAAAATCACACCCCTTCTCTTAATGACCAAACTCTGGAATTTTAAAAATCCC 332
|||
Db 65 CCCTTCAAAAAATCACACCCCTTCTCTTAATGACCAAACTCTGGAATTTTAAAAATCCC 184
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QY 333 GAACGGATCAACAATGCCTTCTTTCTAAATGACCAAACTCTGGAATTTTAAAAATCCC 392
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Db 125 GAACGGATCAACAATGCCTTCTTTCTAAATGACCAAACTCTGGAATTTTAAAAATCCC 184
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QY 393 TTCCACACTTGCACACCCATGGACCCATCTGTGCCCATCTGGATTTATATTTGTTGT 452
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Db 185 TTCCACACTTGCACACCCATGGACCCATCTGTGCCCATCTGGATTTATATTTGTTGT 244
|||
QY 453 GATATTTTGCATCATATAGTTGCAATTGCACTACTGATTTTATCAGGGATCTGGCAACG 512
|||
Db 245 GATATTTTGCATCATATAGTTGCAATTGCACTACTGATTTTATCAGGGATCTGGCAACG 304
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QY 513 TAGAAGAAAGAACAAAGAACCATCTGAAGTGGATGACGCTGAAGATAAGTGTGAAACAT 572
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Db 305 TAGAAGAAAGAACAAAGAACCATCTGAAGTGGATGACGCTGAAGATAAGTGTGAAACAT 364
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QY 573 GATCAAAATTGAAATGGCATCCCTCTGATCCCTTGGACATGAAGGG-GGGCATATTAA 631
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Db 365 GATCAAAATTGAAATGGCATCCCTCTGATCCCTTGGACATGAAGGGAGGCATATTAA 424
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QY 632 TGATGCTTTCATGACAGAGGATGAGAGGCTCACCCCTCTCTGAAAGGCTGTTGTTCTGCT 691
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Db 425 TGATGCTTTCATGACAGAGGATGAGAGGCTCACCCCTCTCTGAAAGGCTGTTGTTCTGCT 484
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QY 692 TCCTCAAGAAATTAACATTTTGTCTGTGTCATCTGTGATCCCTGAGCATCCTGAATACCAAGAG 751
|||
Db 485 TCCTCAAGAAATTAACATTTTGTCTGTGTCATCTGTGATCCCTGAGCATCCTGAATACCAAGAG 544
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QY 752 CAGATCATATATTTTGTCTTCCATCTCTTTTGTGTAATAAATTTTGAATGTCTTGAA 811
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Db 545 CAGACCATATATTTTGTCTTCCATCTCTTTTGTGTAATAAATTTTGAATGTCTTGAA 604
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QY 812 GTGAAAAGCAATCAATTATATCCCAACCAACCACTGAATCATAGCTATTACGACTCA 871
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Db 605 GTGAAAAGCAATCAATTATATCCCAACCAACCACTGAATCATAGCTATTACGACTCA 664
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QY 872 AAATATTTCTAAAAATATTTT-CTGACAGTATAGTGTATAAATGTGTCATGTGTTT 929
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Db 665 NAATATTTCTAAAAATATTTTCTGAAACAGTATTTATGTATAAATGACCGCATGTGTTT 724
|||
QY 930 GTAGTTATTGATTAAAGCAATTTTGTAGAAATAAGATCAGGCATATGTATATTTTTCACAC 989

Db 725 GGAGTATTGAATTAGCATTTTAAATAAGATCAGGCATTGTATATATTTCCACAT 784
 QY 990 TTCAAAGACCTAAGGA 1005
 Db 785 TCAAAAACCAAGGAA 800

RESULT 8
 CA312017/c
 LOCUS
 DEFINITION
 UI-CF-FN0-afj-e-08-0-UI.51 UI-CF-FN0 Homo sapiens cDNA clone
 UI-CF-FN0-afj-e-08-0-UI 3', mRNA sequence.

ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Homo sapiens (human)
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 750)
 Normalization and subtraction: two approaches to facilitate gene
 discovery
 Genome Res. 6 (9), 791-806 (1996)
 97044477
 8889548
 Contact: McCray, PB
 McCray Lab
 University of Iowa
 2024 University of Iowa Med Labs, Iowa City, IA 52242, USA
 Tel: 319 356 4866
 Fax: 319 356 7171
 Email: paul-mccray@uiowa.edu
 Tissue Procurement: Dr. M. J. Welsh, University of Iowa
 cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
 cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Researchers may obtain clones from Research
 Genetics (www.resgen.com) or from Open Biosystems
 (www.openbiosystems.com).
 Seq primer: M13 FORWARD
 POLYA=Yes.

FEATURES
 Source
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 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="UI-CF-FN0-afj-e-08-0-UI"
 /tissue_type="Human Lung Epithelial cells"
 /lab_host="DH10B (Life Technologies) (T1 phage resistant)"
 /clone_lib="UI-CF-FN0"
 /note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a
 modified polylinker; Site 1: EcoR I; Site 2: Not I;
 UI-CF-FN0 is a subtracted cDNA library derived from two
 normalized Human lung epithelial cell libraries (EN1 and
 DUL) The library was subtracted according to according to
 Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
 1996. For additional information, contact:
 bentos-soares@uiowa.edu
 TAG TISSUE=Human Lung Epithelial Cell Lines untreated LPS
 6hr to LPS 24h
 TAG_LIB=UI-CF-FN0
 TAG_SEQ=CTGCTCAGGT"

ORIGIN
 Query Match 53.2%; Score 715.4; DB 14; Length 750;
 Best Local Similarity 98.8%; Pred. No. 4.4e-94;
 Matches 741; Conservative 0; Mismatches 7; Indels 2; Gaps 2;
 QY 598 TCTGATCCCTGGACATGAAGG-GGGCATATTATGATGCTTTCATGACAGGATGAG 656
 Db 750 TCTGATCCNCTGGACATGAAGGAGGGGCATATTATGATGCTTTCATGACAGGATGAG 691

QY 657 AGGCTCACCCCTCTCTGAAGGGCTGTGTTCTGCTTCTCAAGAAATTAACATTTGTTT 716
 Db 690 AGGCTCACCCCTCTCTGAAGGGCTGTGTTCTGCTTCTCAAGAAATTAACATTTGTTT 631
 QY 717 CTGTGTGACTGCTGAGCATCTCTGAATACCAAGAGCAGATCATATATTTGTTTCCCAT 776
 Db 630 CTGTGTGACTGCTGAGCATCTCTGAATACCAAGAGCAGATCATATATTTGTTTCCCAT 571
 QY 777 TCCTCTTTTGTAAATTTTGAATGCTGCTTGAAGTGAAGCAATCAATATATATACCCAC 836
 Db 570 TCCTCTTTTGTAAATTTTGAATGCTGCTTGAAGTGAAGCAATCAATATATATACCCAC 511
 QY 837 CAACACCACCTGAATCATAGCTATTACGACTCAAAATATTCTAAATATTTTCTCTGAC 896
 Db 510 CAACACCACCTGAATCATAGCTATTACGACTCAAAATATTCTAAATATTTTCTCTGAC 451
 QY 897 AGTATAGTGTATAAATGCTGCTCATGCTGTTTGTAGTTTGTAGTTTGTAGTTTGTAG 956
 Db 450 AGTATAGTGTATAAATGCTGCTCATGCTGTTTGTAGTTTGTAGTTTGTAGTTTGTAG 391
 QY 957 AATAAGATCAGGCATATGTATATATTTTTCACACTTCAAGAGCCTTAAGGAAAAATAATTT 1016
 Db 390 AATAAGATCAGGCATATGTATATATTTTTCACACTTCAAGAGCCTTAAGGAAAAATAATTT 331
 QY 1017 TCCAGTGGAGATACATATATATGTTGTAGAAATCAATTTGAAATGATCCTTTTGTGACG 1076
 Db 330 TCCAGTGGAGATACATATATATGTTGTAGAAATCAATTTGAAATGATCCTTTTGTGACG 271
 QY 1077 ATCACTTATATCACTCTGTATATGACTAAGTAAACAAAGTGAGAAATTAATTTGTAAA 1136
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 QY 1137 TGGATGGATAAAATGGAATTAATCTATATACAG-GGTGGAATTTTATCTCTGTTATCACAC 1195
 Db 210 TGGATGGATAAAATGGAATTAATCTATATACAGNGGTGGAATTTTATCTCTGTTATCACAC 151
 QY 1196 CAACAGTTGATTATATATTTTCTGAATATCAGCCCTTAATAGGACAATTTCTATTGTTGA 1255
 Db 150 CAACAGTTGATTATATATTTTCTGAATATCAGCCCTTAATAGGACAATTTCTATTGTTGA 91
 QY 1256 CCATTTCTACAATTTGTAAAGTCCAAATCTGTGCTTAATTAATAAGTAATATCATCTC 1315
 Db 90 CCATTTCTACAATTTGTAAAGTCCAAATCTGTGCTTAATTAATAAGTAATATCATCTC 31
 QY 1316 TTTTAAAAAATAAAAAAAAAAAAAAAAAAAAA 1345
 Db 30 TTTTGTATTGTGAAAAAAAAAAAAAAAAAAAA 1

RESULT 9
 BG429174
 LOCUS
 DEFINITION
 BG429174 NIH_MGC_75 Homo sapiens cDNA clone IMAGE:4612062 5',
 mRNA sequence.
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Homo sapiens (human)
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 780)
 NIH-MGC http://mgs.nci.nih.gov/.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: CLONTECH Laboratories, Inc.
 cDNA Library preparation: CLONTECH Laboratories, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLCMI359 row: 0 column: 07

High quality sequence stop: 718.

Location/Qualifiers

1. 780

/organism="Homo sapiens"

/mol_type="mrna"

/db_xref="taxon:9606"

/clone="IMAGE:4612062"

/lab_host="DH10B (T1 phage-resistant)"

/clone_lib="NIH_MGC_75"

/note="Organ: kidney; Vector: pDNR-LIB (Clontech); Site_1:

SfiI (ggcgcctcgcc); Site_2: SfiI (ggcattatggcc); 5' and

3' adaptors were used in cloning as follows: 5' adaptor

sequence: 5'-CAGGCCATTATGGCC-3' and 3' adaptor sequence:

5'-ATTCTAGAGCGGCGGCGCCGACATG-dt(30)BN-3' (where B = A,

C, or G and N = A, C, G, or T). Average insert size 1.65

kb (range 0.5-4.0 kb). 15/15 colonies contained inserts

by PCR. This library was enriched for full-length clones

and was constructed by Clontech Laboratories (Palo Alto,

CA). Note: this is a NIH_MGC Library."

ORIGIN

Query Match 52.5%; Score 706.8; DB 12; Length 780;

Best Local Similarity 97.4%; Pred. No. 7.4e-93;

Matches 750; Conservative 0; Mismatches 17; Indels 3; Gaps 3;

QY 36 TGCCATTGCTGCTGAACTCTGTCAACCAGGTGCAGAAATGCTTTTAAAGTGAGACTTAG 95
DB 1 TGCCATTGCTGCTGAACTCTGTCAACCAGGTGCAGAAATGCTTTTAAAGTGAGACTTAG 60
QY 96 TATCAGAACAGCTCTGGAGATAAAGCATATGCTGCGATACCAATGAAGAAATACCTCTT 155
DB 61 TATCAGAACAGCTCTGGAGATAAAGCATATGCTGCGATACCAATGAAGAAATACCTCTT 120
QY 156 CAAGCGATGGTAGCTTTCTCCATGAGAAAAGTTCCCAACAGAGAACCAAGAAATTC 215
DB 121 CAAGCGATGGTAGCTTTCTCCATGAGAAAAGTTCCCAACAGAGAACCAAGAAATTC 180
QY 216 CCATGCTCTACTTTTGCAATGTAACCCAGAGGGTATCACTCTGGTTTGTGGTTACAGACCC 275
DB 181 CCATGCTCTACTTTTGCAATGTAACCCAGAGGGTATCACTCTGGTTTGTGGTTACAGACCC 240
QY 276 TTCAAAAATCACACCCCTTCTGCTGTGTGAGGTGCAATCAGCCCATAGAAATGAACAAGAA 335
DB 241 TTCAAAAATCACACCCCTTCTGCTGTGTGAGGTGCAATCAGCCCATAGAAATGAACAAGAA 300
QY 336 CCGGATCAACAATGCCCTTCTTCTAAATGACCAAACTCTGGAATTTTAAAAATCCCTTC 395
DB 301 CCGGATCAACAATGCCCTTCTTCTAAATGACCAAACTCTGGAATTTTAAAAATCCCTTC 360
QY 396 CACACTTGACACCCCATGGACCCCATCTGTGCCCATCTGGATTATTATATTGGTGAT 455
DB 361 CACACTTGACACCCCATGGACCCCATCTGTGCCCATCTGGATTATTATATTGGTGAT 420
QY 456 ATTTTGCATCATATAGTTTGAATTTGCAATTTGCACTACTGATTTTATCAGGGATCTGGCAACGTAG 515
DB 421 ATTTTGCATCATATAGTTTGAATTTGCAATTTGCACTACTGATTTTATCAGGGATCTGGCAACGTAG 480
QY 516 AAGAAAGAACAAAGAACCATCTGAAGTGGATGACCGTGAAGATAAGTGTGAAGAACATGAT 575
DB 481 AAGAAAGAACAAAGAACCATCTGAAGTGGATGACCGTGAAGATAAGTGTGAAGAACATGAT 540
QY 576 CACAATTGAAATGGCATCCCTCTGATCCCTGGACATGAGGG -GGGCATATTAATGA 634
DB 541 CACAATTGAAATGGCATCCCTCTGATCCCTGGACATGAGGGAGGGCATATTAATGA 600
QY 635 TGCCTTCATGACAGAGGATGAGGGCTC -ACCCCTCTCTGAGGGCTGTGTTCTGCTTC 693
DB 601 TGCCTTCATGACAGACGATGAGGGCTCAACCCCTCTCTGAGGGCTGTGTTCTGCTTC 660
QY 694 CTCAGAAATTAACAATTTGTTTCTGT -GTGACTGCTGAGCATCTCTGAATACCAAGAGC 752

DB 661 CTCAGGAATTAACATTTGTTCTCTGGTGACTTGTGAGCATCTCTGAATACCAAGAGC 720
QY 753 AGATCATATATTTGTTTTCACCATCTCTCTTTTGTAAATAAATTTTGAATG 802
DB 721 AGATCATATATTTGTTTTCACCAATCTCTCTTTTGTAAATAAATTTTGGATG 770
RESULT 10
BG181765
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 754)
Harrington, J.J., Sherf, B., Rundlett, S., Jackson, P.D., Perry, R.,
Cain, S., Leventhal, C., Thornton, M., Ramchandran, R.,
Whittington, J., Lerner, L., Costanzo, D., McElligott, K., Booser, S.,
Mays, R., Smith, B., Veloso, N., Klika, A., Hess, J., Cothren, K., Lo, K.,
Offenbacher, J., Danzig, J. and Ducar, M.
Creation of genome-wide protein expression libraries using random
activation of gene expression
Nat. Biotechnol. 19 (5), 440-445 (2001)
21227151
11329013
Contact: Scott J. Cain
Athersys, Inc.
3201 Carnegie Ave, Cleveland, OH 44115, USA
Tel: 216 431 9900
Fax: 216 361 9596
Email: scain@athersys.com
High quality sequence stop: 548.
Location/Qualifiers
1. 754
/organism="Homo sapiens"
/mol_type="mrna"
/db_xref="taxon:9606"
/cell_line="HT1080"
/clone_lib="Athersys RAGE Library"
/note="See 'Creation of Genome-wide Protein Expression
Libraries using Random Activation of Gene Expression',
Nature Biotechnology, in press. Note that even though the
cell type indicated is HT1080, since a random activation
method was used, these sequence tags are not necessarily
expressed in HT1080 under normal circumstances."
ORIGIN
Query Match 52.3%; Score 704.4; DB 12; Length 754;
Best Local Similarity 97.7%; Pred. No. 1.7e-92;
Matches 725; Conservative 0; Mismatches 16; Indels 1; Gaps 1;
QY 217 CATGTCTACTTTTGCAATGTAACCCAGAGGGTATCACTCTGGTTTGTGGTTACAGACCCCT 276
DB 11 CCTGTCTACTTTTTCATGTAACCCACAGGGTATCACTCTGGTTTGTGGTTACAGACCCCT 70
QY 277 TCAAAAATCACACCCCTTCTCTGCTGTGTGAGGTGCAATCAGCCATAAGAAATGAACAAGAAC 336
DB 71 TCAAAAATCACACCCCTTCTCTGCTGTGTGAGGTGCAATCAGCCATAAGAAATGAACAAGAAC 130
QY 337 CGGATCAACAATGCCCTTCTTTCTAAATGACCAAACTCTGGAATTTTAAAAATCCCTTCC 396
DB 131 CGGATCAACAATGCCCTTCTTTCTAAAGATCAAACTCTGGAATTTTAAAAATCCCTTCC 190
QY 397 ACACCTTGACACCCCATGGACCCCATCTGTGCCCATCTGGATTATTATATTGGTGATGA 456
DB 191 ACACCTTGACACCCCATGGACCCCATCTGTGCCCATCTGGATTATTATATTGGTGATGA 250
QY 457 TTTTGCATCATATAGTTTGAATTTGCATCTGACTACTGATTTTATCAGGGATCTGGCAACGTAGA 516

Db 251 TTTTGCATCATCATAGTTGCAATTCACACTACTGATTTTATCAGGATCTGGCAACGTAGA 310
Qy 517 AGAAAGAACAAAGAACCATCTGAAGTGGATGAGCGCTGAAGATAAGTGTGAAACATGATC 576
Db 311 AGAAAGAACAAAGAACCATCTGAAGTGGATGAGCGCTGAAGATAAGTGTGAAACATGATC 370
Qy 577 ACAATTGAAATGCGCATCCCTCTGATCCCTCGATCCCTCGACATGAAGG-GGGCATATTAATGAT 635
Db 371 TCAATTGAAATGCGCATCCCTCTGATCCCTCGACATGAAGGAGGGGCATATTAATGAT 430
Qy 636 GCCTTCATGACAGAGGATGAGAGGCTCACCCCTCTCTGAAGGCTGTTGTTCTGCTTCCT 695
Db 431 GCCTTCATGACAGAGGATGAGAGGCTCACCCCTCTCTGAAGGCTGTTGTTCTGCTTCCT 490
Qy 696 CAAGAAATTAAACATTTGTTCTGCTGACTGCTGAGCATCTCTGAATGCTTGAAGTGA 755
Db 491 CAAAAAATTAAACATTTGTTCTGCTGACTGCTGAGCATCTCTGAATGCTTGAAGTGA 550
Qy 756 TCATATATTTTGTTCACCATTTCTCTTTTGTAAATAAATTTGAATGCTTGAAGTGA 815
Db 551 TCATATATTTTGTTCACCATTTCTCTTTTGTAAATAAATTTGAATGCTTGAAGTGA 610
Qy 816 AAAGCAATCAATTATACCCACCAACACCACTGAATCATAGTATTTCACGACTCAAAAT 875
Db 611 AAAGCAATCAATTATACCCACCAACACCACTGAATCATAGTATTTCACGACTCAAAAT 670
Qy 876 ATTCTAAATATTTTCTGACAGTATAGTGATATAAATGTGGTATGTTGTTGTTGTTGTT 935
Db 671 ATTCTAAATATTTTCTGACAGTATAGTGATATAAATGTGGCATTGTTGTTGTTGTTGTT 730
Qy 936 ATTGATTTAAGCATTTTGTAGAA 957
Db 731 ATTGATTTAAGCATTTTGTAGAA 752

RESULT 11
BG400845
LOCUS
DEFINITION BG400845 792 bp mRNA linear EST 12-MAR-2001
602464068F1 NIH_MGC_75 Homo sapiens cDNA clone IMAGE:4592296 5',
mRNA sequence.
ACCESSION BG400845
VERSION BG400845.1 GI:13294293
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 792)
TITLE NIH-MGC http://mgi.nci.nih.gov/.
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cga@bbs-rcmail.nih.gov
Tissue Procurement: CLONTECH Laboratories, Inc.
CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCMI330 row: 9 column: 17
High quality sequence stop: 784.
Location/Qualifiers
1. .792
/organism="Homo sapiens"
/mol_type="mRNA"
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/clone="IMAGE:4592296"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NIH_MGC_75"
/note="Organ: kidney; Vector: pDNR-LIB (Clontech); Site 1:
SfiI (ggccgctcgcc); Site_2: SfiI (ggccattatggcc); 5' and

FEATURES
source

3' adaptors were used in cloning as follows: 5' adaptor
sequence: 5'-CAGGCCATTATGCC-3' and 3' adaptor sequence:
5'-ATTCTAGAGCGCGGCGGCATG-dt(30)BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size 1.65
kb (range 0.5-4.0 kb). 15/15 colonies contained inserts
by PCR. This library was enriched for full-length clones
and was constructed by Clontech Laboratories (Palo Alto,
CA). Note: this is a NIH_MGC Library."

ORIGIN

Query Match 51.6%; Score 695.2; DB 12; Length 792;
Best Local Similarity 98.0%; Pred. No. 3.5e-91;
Matches 747; Conservative 0; Mismatches 8; Indels 7; Gaps 4;
Qy 1 GAAAGAAATGTTGCTGCTCTTTTCTGCTGACTGCCATTTCATGCTGAACTCTGTCAA 60
Db 26 GAAAGAAATGTTGCTGCTCTTTTCTGCTGACTGCCATTTCATGCTGAACTCTGTCAA 85
Qy 61 CCAGGTGCAGAAATGCTTTTAAAGTGAGACTTTAGTATCAGAACAGCTCTGGGAGATAAA 120
Db 86 CCAGGTGCAGAAATGCTTTTAAAGTGAGACTTTAGTATCAGAACAGCTCTGGGAGATAAA 145
Qy 121 GCATATGCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGCTTTCTCCATG 180
Db 146 GCATATGCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGCTTTCTCCATG 205
Qy 181 AGAAAGTTCCCAACAGAGAACCAACAGAAATTTCCCATGCTTCTTCAATGTAACC 240
Db 206 AGAAAGTTCCCAACAGAGAACCAACAGAAATTTCCCATGCTTCTTCAATGTAACC 265
Qy 241 CAGAGGGTATCATTTCTGTTGTTGTTTACAGACCTTCAAAAAATCACACCTTCCCTGCT 300
Db 266 CAGAGGGTATCATTTCTGTTGTTGTTTACAGACCTTCAAAAAATCACACCTTCCCTGCT 325
Qy 301 GTTGAGGTGCAATCAGCCATGAAGAATGAACAGAACCGGATCAACAATGCCCTTCTTCTA 360
Db 326 GTTGAGGTGCAATCAGCCATGAAGAATGAACAGAACCGGATCAACAATGCCCTTCTTCTA 385
Qy 361 AATGACCAAACTCTGGAATTTTAAAAATCCCTTCCACACTTGACCCACCCATGGACCCA 420
Db 386 AATGACCAAACTCTGGAATTTTAAAAATCCCTTCCACACTTGACCCACCCATGGACCCA 445
Qy 421 TCTGTGCCCATCTGGATTTATATATTTTGGTGTGATATTTTGCATCATCATAGTTGCAATT 480
Db 446 TCTGTGCCCATCTGGATTTATATATTTTGGTGTGATATTTTGCATCATCATAGTTGCAATT 505
Qy 481 GCACTACTGATTTTATCAGGATCTGGCAACGTAGAAGAACAAAGAACCATCTGAA 540
Db 506 GCACTACTGATTTTATCAGGATCTGGCAACGTAGAAGAACAAAGAACCATCTGAA 565
Qy 541 GTGGATGCGCTGAAGATAAGTGTGAAACATGATCACAATTTGAAAATGGCATCCCTCT 600
Db 566 GTGGATGCGCTGAAGATAAGTGTGAAACATGATCACAATTTGAAAATGGCATCCCTCT 625
Qy 601 GATCCCTGGACATGAAGGG---GGGCATATTAATGATGCCCTTCA-TGACAGAGGATGAG 656
Db 626 GATCCCTGGACATGAAGGGAGCGGCATATTAATGATGCCCTTCA-TGACAGAGGATGAG 685
Qy 657 AGGCTCACCCTCTCTGAAGGGCTGTTGTTCTGCTG-TTCCTCAAGAAATT--AAACATTG 713
Db 686 AGGCTCACCCTCTCTGAAGGGCTGTTGTTCTGCTG-TTCCTCAAGAAATT--AAACATTG 745
Qy 714 TTTCTGTGCTGCTGCTGAGCATCTTGAATACCAAGAGCAGA 755
Db 746 TTTCTGTGCTGCTGCTGAGCATCTTGAATACCAAGAGCAGA 787

RESULT 12
BG400319
LOCUS
DEFINITION BG400319 791 bp mRNA linear EST 12-MAR-2001
602464526F1 NIH_MGC_75 Homo sapiens cDNA clone IMAGE:4592575 5',
mRNA sequence.
ACCESSION BG400319

Matches	715;	Conservative	0;	Mismatches	22;	Indels	6;	Gaps	3;
Qy	61	CCAGGTGCAGAAATGCTTTTAAAGTCAGACTTAGTATCAGAACAGCTCTGGGAGATAAA	120						
Db	165	CGAGGTGCAGAAATGCTTTTAAAGTCAGACTTAGTATCAGAACAGCTCTGGGAGATAAA	224						
Qy	121	GCATATGCCTGGGATACCAATGAAGATACCTCTTCAAGCGATGGTAGCTTCTCCATG	180						
Db	225	GCATATGCCTGGGATACCAATGAAGATACCTCTTCAAGCGATGGTAGCTTCTCCATG	284						
Qy	181	AGAAAAGTCCCAACAGAGAGCAAGCAAGAAATTTCCCATGTCCTACTTTGCAATGTAACC	240						
Db	285	AGAAAAGTCCCAACAGAGAGCAAGCAAGAAATTTCCCATGTCCTACTTTGCAATGTAACC	344						
Qy	241	CAGAGGTATCATCTCTGTTTGTGGTTACAGACCTTCAAAAAATCACACCCCTTCTGCT	300						
Db	345	CAGAGGTATCATCTCTGTTTGTGGTTACAGACCTTCAAAAAATCACACCCCTTCTGCT	404						
Qy	301	GTTGAGGTGCAATCAGCCATAGATGAACAGAACCGGATCAACAAATGCCCTTCTTCTA	360						
Db	405	GTTGAGGTGCAATCAGCCATAGATGAACAGAACCGGATCAACAAATGCCCTTCTTCTA	464						
Qy	361	AATGACCAAACTCTGGAATTTTAAATAATCCCTTCCACACTTGCACACCCATGACCCA	420						
Db	465	AATGACCAAACTCTGGAATTTTAAATAATCCCTTCCACACTTGCACACCCATGACCCA	524						
Qy	421	TCTGTGCCCATCTGGAATTTATATTTGGTGTGATATTTTGCATCATATGTTGCAATT	480						
Db	525	TCTGTGCCCATCTGGAATTTATATTTGGTGTGATATTTTGCATCATATGTTGCAATT	584						
Qy	481	GCACTACTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGCAAAAGAACCAATCTGAA	540						
Db	585	GCACTACTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGCAAAAGAACCAATCTGAA	644						
Qy	541	GTGATGACGCTGAAGATAAGTGTGAATAACATGATCAAAATGGAATGGCATCCCTCT	600						
Db	645	GTGATGACGCTGAAGATAAGTGTGAATAACATGATCAAAATGGAATGGCATCCCTCT	704						
Qy	601	GATCCCTCGACATGAAGGG-GGGCATATTAATGATGCCCTTCAAGAAATTAACATTTGTTT	659						
Db	705	GATCCCTCGACATGAAGGGAGGGCATATTAATGATGCCCTTCAAGAAATTAACATTTGTTT	764						
Qy	660	CTCACCCCCTCTCTGAAAGGGCTGTGTTCTGCTTCCCTCCAGAAATTAACATTTGTTT	717						
Db	765	CTCACCCCCTCTCTGAAAGGGCTGTGTTCTGCTTCCCTCCAGAAATTAACATTTGTTT	824						
Qy	718	TGTTGACTGCTGAGCATCTGAAATACCAAGAGCAGATCATATTTTGTGTTT---CAC	774						
Db	825	TGTTGACTGCTGAGCATCTGAAATACCAAGAGCAGATCATATTTTGTGTTT---CAC	884						
Qy	775	ATTCTCTTTTGTGAATAAATTTT	797						
Db	885	TTCTCTCTTTTGGAAATAAATTT	907						

RESULT 14
BG427247
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

BG427247 855 bp mRNA linear EST 14-MAR-2001
602494304F1 NIH_MGC_75 Homo sapiens cDNA clone IMAGE:4608048 5',
mRNA sequence.
BG427247
BG427247.1 GI:13333753
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 855)
NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov

Tissue Procurement: CLONTECH Laboratories, Inc.
cDNA Library Preparation: CLONTECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Plate: LCM1349 row: h column: 01
High quality sequence stop: 735.
Location/Qualifiers
1. .855
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4608048"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NIH_MGC_75"
/note="Organ: kidney; Vector: pDNR-LIB (Clontech); Site 1: SfiI (ggccattatggcc); Site 2: SfiI (ggccattatggcc); 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGCCATTATGGCC-3' and 3' adaptor sequence: 5'-ATTCTAGAGCGCGGCGGACATG-dT(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.65 kb (range 0.5-4.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH_MGC Library."

ORIGIN

Query Match 49.2%; Score 661.6; DB 12; Length 855;
Best Local Similarity 95.2%; Pred. No. 2.3e-86;
Matches 769; Conservative 0; Mismatches 29; Indels 10; Gaps 8;

Qy	1	GAAAGAATGTTGGCTGCTCTTTTCTGTTGCTGCTGCCATTTCATGCTGAACTCTGTCAA	60
Db	27	GAAAGAATGTTGGCTGCTCTTTTCTGTTGCTGCTGCCATTTCATGCTGAACTCTGTCAA	86
Qy	61	CCAGGTGCAGAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAA	120
Db	87	CCAGGTGCAGAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAA	146
Qy	121	GCATATGCCTGGGATACCAATGAAGATACCTCTTCAAGCGATGGTAGCTTTCTCCATG	180
Db	147	GCATATGCCTGGGATACCAATGAAGATACCTCTTCAAGCGATGGTAGCTTTCTCCATG	206
Qy	181	AGAAAAGTTCCTCAACAGAGAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACC	240
Db	207	AGAAAAGTTCCTCAACAGAGAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACC	266
Qy	241	CAGAGGGTATCATTTCTGTTTGTGTTTACAGACCTTCAAAAAATCACACCCCTTCTGCT	300
Db	267	CAGAGGGTATCATTTCTGTTTGTGTTTACAGACCTTCAAAAAATCACACCCCTTCTGCT	326
Qy	301	GTTGAGGTGCAATCAGCCATAGAAATGAACAAGAACCGGATCAACAAATGCCCTTCTTCTA	360
Db	327	GTTGAGGTGCAATCAGCCATAGAAATGAACAAGAACCGGATCAACAAATGCCCTTCTTCTA	386
Qy	361	AATGACCAAACTCTGGAATTTTAAATAATCCCTTCCACACTTGCACACCCATGGAACCA	420
Db	387	AATGACCAAACTCTGGAATTTTAAATAATCCCTTCCACACTTGCACACCCATGGAACCA	446
Qy	421	TCTGTGCCCATCTGGATTTATATTTGGTGTGATATTTTGCATCATATGTTGCAATT	480
Db	447	TCTGTGCCCATCTGGATTTATATTTGGTGTGATATTTTGCATCATATGTTGCAATT	506
Qy	481	GCACTACTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAAC-AAAGAACCATCTGA	539
Db	507	GCACTACTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGA	566
Qy	540	AGTGGATGACGCTGAAGATAAGTGTGAAAAACATGATCACAATTTGAAAAATGGCATCCCTC	599
Db	567	AGTGGATGACGCTGAAGAT-AGTGTGAAAAACATGATCACAATTTGAAAAATGGCATCCCTC	625

QY 600 TGATCCCTGGACATGAAGGG-GGGCATTAATGATGCTTTCATGAC-AGAGGATGAGA 657
Db 626 TGATCCCTGGACATGAAGGGAGGGCATTAATGATGCTTTCATGACAAAGAGGATGAGA 685
QY 658 GGCTCA-CCCCTCTCTGAAGGGCTGTTGTTCTGCTTCCCTCAAGAAATTAACAATTGTTT 716
Db 686 GGCTCACCCCTCTCTGAAGGGCTGTTGTTCTGCTTCCCTCAAGAAATTA-ACATTGTT 742
QY 717 CTGTGTGACTGTGAGCATCTGAAATACCAAGAGCAGATCATATATTTGTTTCCACCAT 776
Db 743 CTGTGTGACTG-TGAGCATCTTTAAAAACCAAGAGC-GATTATATATTTGTTTCCCATCT 800
QY 777 TCTTCTTTTGTAAATAAAATTTGAATGTG 804
Db 801 TCTTGTAAATCTTTTGATGTGCTAAAGTG 828

RESULT 15
AY399636
LOCUS
DEFINITION Homo sapiens HCM0290 gene, VIRTUAL TRANSCRIPT, partial sequence,
genomic survey sequence.
ACCESSION AY399636
VERSION AY399636.1 GI:39755625
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 669)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE 2 (bases 1 to 669)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering
them based on alignment.
FEATURES
source Location/Qualifiers
1..669
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/db_xref="taxon:9606"
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ORIGIN
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Best Local Similarity 99.9%; Pred. No. 1.2e-85;
Matches 568; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
QY 7 ATGTTGTGGCTGCTCTTTTCTGGTGACTGCCATTCAATGCTGAACCTCTGTCAACCAGGT 66
Db 1 ATGTTGTGGCTGCTCTTTTCTGGTGACTGCCATTCAATGCTGAACCTCTGTCAACCAGGT 60
QY 67 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 126
Db 61 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 120
QY 127 GCCTGGGATACCAATGAAGATACCTCTTCAAGCGATGGTAGCTTTCTCCATGAGAAA 186
Db 121 GCCTGGGATACCAATGAAGATACCTCTTCAAGCGATGGTAGCTTTCTCCATGAGAAA 180

QY 187 GTTCCCAACAGAGAAAGCAACAGAAATTTCCCATGTCTCTACTTTGCAATGTAACCCAGAGG 246
Db 181 GTTCCCAACAGAGAAAGCAACAGAAATTTCCCATGTCTCTACTTTGCAATGTAACCCAGAGG 240
QY 247 GTATCAATCTGGTTTGTGGTTTACAGACCTTTCAAAAAATCACACCTTCTCTGCTGTTGAG 306
Db 241 GTATCAATCTGGTTTGTGGTTTACAGACCTTTCAAAAAATCACACCTTCTCTGCTGTTGAG 300
QY 307 GTGCAATCAGCCCATAGAATGAACCAAGAACCGGATCAACAATGCCCTTCTTTCTAAATGAC 366
Db 301 GTGCAATCAGCCCATAGAATGAACCAAGAACCGGATCAACAATGCCCTTCTTTCTAAATGAC 360
QY 367 CAAACTCTGGAAATTTTAAAAAATCCCTTCCACACTTGCAACCCCATGGACCCCATCTGTG 426
Db 361 CAAACTCTGGAAATTTTAAAAAATCCCTTCCACACTTGCAACCCCATGGACCCCATCTGTG 420
QY 427 CCCATCTGGATTAATATATTTGGTGTGATATTTTGCAATCATATGCAATTGCACTA 486
Db 421 CCCATCTGGATTAATATATTTGGTGTGATATTTTGCAATCATATGCAATTGCACTA 480
QY 487 CTGATTTTATCAGGGATCTGGCAACCGTAGAAGAAAGAACAAAGAACCATCTGAAAGTGGAT 546
Db 481 CTGATTTTATCAGGGATCTGGCAACCGTAGAAGAAAGAACAAAGAACCATCTGAAAGTGGAT 540
QY 547 GACGCTGAAGATAAGTGTGAAAAACATGATCACAATTTGAAAATGGCATCCCTCTGATCCC 606
Db 541 GACGCTGAAGATAAGTGTGAAAAACATGATCACAATTTGAAAATGGCATCCCTCTGATCCC 600
QY 607 CTGGACATGAAGGG-GGGCATATTAATGATGCCCTTTCATGACAGAGGATGAGAGGCTCACC 665
Db 601 CTGGACATGAAGGGAGGGGCATATTAATGATGCCCTTTCATGACAGAGGATGAGAGGCTCACC 660
QY 666 CCTCTCTGA 674
Db 661 CCTCTCTGA 669

Search completed: April 3, 2004, 23:26:53
Job time : 3975 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 31, 2004, 12:01:04 ; Search time 60 Seconds
(without alignments)
998.335 Million cell updates/sec

Title: US-09-989-724-387
Perfect score: 1102
Sequence: 1 MLWLLFLVTAIHAELCPG.....ENGIPSDPLDMKGGILMMP 212

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04.*
1: Geneseqp1980s.*
2: Geneseqp1990s.*
3: Geneseqp2000s.*
4: Geneseqp2001s.*
5: Geneseqp2002s.*
6: Geneseqp2003as.*
7: Geneseqp2003bs.*
8: Geneseqp2004s.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	1102	100.0	212	3	AAY66751	Membrane-
2	1102	100.0	212	3	AAB33447	Human PRO
3	1102	100.0	212	3	AAB24430	Human PRO
4	1102	100.0	212	4	AAU12412	Human PRO
5	1102	100.0	212	4	AAB65274	Human PRO
6	1102	100.0	212	6	ABU58089	Human PRO
7	1102	100.0	212	6	ABU59167	Novel hum
8	1102	100.0	212	6	ABU82679	Human sec
9	1102	100.0	212	6	ABO17856	Novel hum
10	1102	100.0	212	6	ABU60598	Human sec
11	1102	100.0	212	6	ABU13980	Human PRO
12	1102	100.0	212	6	ABU81110	Human PRO
13	1102	100.0	212	6	ABU72565	Novel hum
14	1102	100.0	212	6	ABU66810	Human PRO
15	1102	100.0	212	6	ABU59891	Novel sec
16	1102	100.0	212	6	ABU59314	Human sec
17	1102	100.0	212	6	ABO26011	Human PRO
18	1102	100.0	212	6	ABO25081	Human sec
19	1102	100.0	212	6	ABU59020	Human sec
20	1102	100.0	212	6	ABU92398	Novel hum
21	1102	100.0	212	6	ABU59463	Novel hum
22	1102	100.0	212	6	ABU67086	Human sec
23	1102	100.0	212	6	ABU92229	Novel hum
24	1102	100.0	212	6	ABU10935	Human PRO
25	1102	100.0	212	6	ABU81687	Novel hum

26	1102	100.0	212	6	ABU88626	Human sec
27	1102	100.0	212	6	ABO34140	Human PRO
28	1102	100.0	212	6	ADA46001	Novel hum
29	1102	100.0	212	6	ADA76432	Human PRO
30	1102	100.0	212	6	ADA19082	Human PRO
31	1102	100.0	212	6	ADA61705	Homo sapi
32	1102	100.0	212	6	ADB19490	Novel hum
33	1102	100.0	212	6	ADB28031	Human PRO
34	1102	100.0	212	6	ADA86510	Novel hum
35	1102	100.0	212	6	ADB16074	Human PRO
36	1102	100.0	212	6	ADA37898	Human sec
37	1102	100.0	212	6	ADA47860	Human PRO
38	1102	100.0	212	6	ADA21584	Human sec
39	1102	100.0	212	6	ADA10371	Human sec
40	1102	100.0	212	6	ADA67655	Human PRO
41	1102	100.0	212	6	ADB30662	Human PRO
42	1102	100.0	212	6	ADA85958	Novel hum
43	1102	100.0	212	6	ADA17915	Human PRO
44	1102	100.0	212	6	ADA97170	Human PRO
45	1102	100.0	212	6	ADA79474	Human PRO

ALIGNMENTS

RESULT 1
AAY66751
ID AAY66751 standard; protein; 212 AA.
XX
AC AAY66751;
XX
DT 05-APR-2000 (first entry)
XX
DE Membrane-bound protein PRO1312.
XX
KW Membrane-bound polypeptide; PRO polypeptide; LDL receptor; TIE ligand;
KW pharmaceutical; receptor immunoadhesin; gene mapping.
XX
OS Homo sapiens.
XX
PN WO9963088-A2.
XX
PD 09-DEC-1999.
XX
PF 02-JUN-1999; 99WO-US012252.
XX
PR 02-JUN-1998; 98US-0087607P.
PR 02-JUN-1998; 98US-0087609P.
PR 02-JUN-1998; 98US-0087759P.
PR 03-JUN-1998; 98US-0087827P.
PR 04-JUN-1998; 98US-0088021P.
PR 04-JUN-1998; 98US-0088025P.
PR 04-JUN-1998; 98US-0088028P.
PR 04-JUN-1998; 98US-0088029P.
PR 04-JUN-1998; 98US-0088030P.
PR 04-JUN-1998; 98US-0088033P.
PR 04-JUN-1998; 98US-0088326P.
PR 05-JUN-1998; 98US-0088167P.
PR 05-JUN-1998; 98US-0088202P.
PR 05-JUN-1998; 98US-0088212P.
PR 05-JUN-1998; 98US-0088217P.
PR 09-JUN-1998; 98US-0088655P.
PR 10-JUN-1998; 98US-0088722P.
PR 10-JUN-1998; 98US-0088730P.
PR 10-JUN-1998; 98US-0088734P.
PR 10-JUN-1998; 98US-0088738P.
PR 10-JUN-1998; 98US-0088740P.
PR 10-JUN-1998; 98US-0088741P.
PR 10-JUN-1998; 98US-0088742P.
PR 10-JUN-1998; 98US-0088810P.
PR 10-JUN-1998; 98US-0088811P.
PR 10-JUN-1998; 98US-0088824P.
PR 10-JUN-1998; 98US-0088825P.

PR 10-JUN-1998; 98US-0088826P.
PR 11-JUN-1998; 98US-0088858P.
PR 11-JUN-1998; 98US-0088861P.
PR 11-JUN-1998; 98US-0088863P.
PR 11-JUN-1998; 98US-0088876P.
PR 12-JUN-1998; 98US-0089090P.
PR 12-JUN-1998; 98US-0089105P.
PR 16-JUN-1998; 98US-0089440P.
PR 16-JUN-1998; 98US-0089512P.
PR 16-JUN-1998; 98US-0089514P.
PR 17-JUN-1998; 98US-0089532P.
PR 17-JUN-1998; 98US-0089538P.
PR 17-JUN-1998; 98US-0089598P.
PR 17-JUN-1998; 98US-0089599P.
PR 17-JUN-1998; 98US-0089600P.
PR 17-JUN-1998; 98US-0089653P.
PR 18-JUN-1998; 98US-0089801P.
PR 18-JUN-1998; 98US-0089907P.
PR 18-JUN-1998; 98US-0089908P.
PR 19-JUN-1998; 98US-0089947P.
PR 19-JUN-1998; 98US-0089948P.
PR 19-JUN-1998; 98US-0089952P.
PR 22-JUN-1998; 98US-0090246P.
PR 22-JUN-1998; 98US-0090252P.
PR 22-JUN-1998; 98US-0090254P.
PR 23-JUN-1998; 98US-0090349P.
PR 23-JUN-1998; 98US-0090355P.
PR 24-JUN-1998; 98US-0090429P.
PR 24-JUN-1998; 98US-0090431P.
PR 24-JUN-1998; 98US-0090435P.
PR 24-JUN-1998; 98US-0090444P.
PR 24-JUN-1998; 98US-0090445P.
PR 24-JUN-1998; 98US-0090461P.
PR 24-JUN-1998; 98US-0090472P.
PR 24-JUN-1998; 98US-0090535P.
PR 24-JUN-1998; 98US-0090538P.
PR 24-JUN-1998; 98US-0090540P.
PR 24-JUN-1998; 98US-0090557P.
PR 25-JUN-1998; 98US-0090676P.
PR 25-JUN-1998; 98US-0090678P.
PR 25-JUN-1998; 98US-0090688P.
PR 25-JUN-1998; 98US-0090690P.
PR 25-JUN-1998; 98US-0090691P.
PR 25-JUN-1998; 98US-0090694P.
PR 25-JUN-1998; 98US-0090695P.
PR 25-JUN-1998; 98US-0090696P.
PR 26-JUN-1998; 98US-0090862P.
PR 26-JUN-1998; 98US-0090863P.
PR 01-JUL-1998; 98US-0091358P.
PR 01-JUL-1998; 98US-0091360P.
PR 02-JUL-1998; 98US-0091478P.
PR 02-JUL-1998; 98US-0091486P.
PR 02-JUL-1998; 98US-0091519P.
PR 02-JUL-1998; 98US-0091544P.
PR 02-JUL-1998; 98US-0091626P.
PR 02-JUL-1998; 98US-0091628P.
PR 02-JUL-1998; 98US-0091633P.
PR 02-JUL-1998; 98US-0091646P.
PR 02-JUL-1998; 98US-0091673P.
PR 07-JUL-1998; 98US-0091978P.
PR 07-JUL-1998; 98US-0091982P.
PR 09-JUL-1998; 98US-0092182P.
PR 10-JUL-1998; 98US-0092472P.
PR 20-JUL-1998; 98US-0093339P.
PR 30-JUL-1998; 98US-0094651P.
PR 04-AUG-1998; 98US-0095282P.
PR 04-AUG-1998; 98US-0095285P.
PR 04-AUG-1998; 98US-0095301P.
PR 04-AUG-1998; 98US-0095302P.
PR 04-AUG-1998; 98US-0095318P.
PR 04-AUG-1998; 98US-0095321P.
PR 04-AUG-1998; 98US-0095325P.
PR 10-AUG-1998; 98US-0095916P.

PR 10-AUG-1998; 98US-0095929P.
PR 10-AUG-1998; 98US-0096012P.
PR 11-AUG-1998; 98US-0096143P.
PR 11-AUG-1998; 98US-0096146P.
PR 12-AUG-1998; 98US-0096329P.
PR 17-AUG-1998; 98US-0096757P.
PR 17-AUG-1998; 98US-0096766P.
PR 17-AUG-1998; 98US-0096768P.
PR 17-AUG-1998; 98US-0096773P.
PR 17-AUG-1998; 98US-0096791P.
PR 17-AUG-1998; 98US-0096867P.
PR 17-AUG-1998; 98US-0096891P.
PR 17-AUG-1998; 98US-0096894P.
PR 17-AUG-1998; 98US-0096895P.
PR 17-AUG-1998; 98US-0096897P.
PR 18-AUG-1998; 98US-0096949P.
PR 18-AUG-1998; 98US-0096950P.
PR 18-AUG-1998; 98US-0096959P.
PR 18-AUG-1998; 98US-0096960P.
PR 18-AUG-1998; 98US-0097022P.
PR 19-AUG-1998; 98US-0097141P.
PR 20-AUG-1998; 98US-0097218P.
PR 24-AUG-1998; 98US-0097661P.
PR 26-AUG-1998; 98US-0097951P.
PR 26-AUG-1998; 98US-0097952P.
PR 26-AUG-1998; 98US-0097954P.
PR 26-AUG-1998; 98US-0097955P.
PR 26-AUG-1998; 98US-0097971P.
PR 26-AUG-1998; 98US-0097974P.
PR 26-AUG-1998; 98US-0097978P.
PR 26-AUG-1998; 98US-0097979P.
PR 26-AUG-1998; 98US-0097986P.
PR 26-AUG-1998; 98US-0098014P.
PR 31-AUG-1998; 98US-0098525P.
PR 16-SEP-1998; 98US-0100634P.
PR 12-JAN-1999; 99US-0115565P.

XX (GETH) GENENTECH INC.

PA Baker K, Chen J, Goddard A, Gurney AL, Smith V, Watanabe CK;
PI Wood WI, Yuan J;

XX WPI; 2000-072883/06.
DR N-PSDB; AAZ65097.

XX Membrane-bound proteins and related nucleotide sequences.

XX Claim 12; Fig 278; 822pp; English.

XX The invention provides membrane-bound PRO polypeptides and
CC polynucleotides encoding them. The PRO sequences of the invention were
CC identified based on extracellular domain homology screening. The PRO
CC sequences have homology with proteins including LDL receptors, TIE
CC ligands and various enzymes. The membrane-bound proteins and receptor
CC immunoadhesins, for instance, can be used as therapeutic agents to block
CC receptor-ligand interactions. The membrane-bound proteins can also be
CC employed for screening of potential peptide or small molecule inhibitors
CC of the relevant receptor/ligand interaction. The PRO encoding sequences
CC are useful as hybridization probes, in chromosome and gene mapping and in
CC the generation of antisense RNA and DNA. PRO nucleic acid sequences will
CC also be useful for the preparation of PRO polypeptides, especially by
CC recombinant techniques

XX SQ Sequence 212 AA;

Query Match 100.0%; Score 1102; DB 3; Length 212;
Best Local Similarity 100.0%; Pred. No. 5.8e-114;
Matches 212; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLWLLFFLVTAIHAELCQPGAENAFKRLSIRLTALGDKAYAWDTNEEYLFKAMVAFSMRK 60
Db 1 MLWLLFFLVTAIHAELCQPGAENAFKRLSIRLTALGDKAYAWDTNEEYLFKAMVAFSMRK 60

QY 61 VNREATEISHVLLCNVTQVSFWFVVTDPKNTLPAVEVQSAIRMNKNRINNAPFLND 120
DB 61 VNREATEISHVLLCNVTQVSFWFVVTDPKNTLPAVEVQSAIRMNKNRINNAPFLND 120
QY 121 QTLFELKIPSTLAPMDPSVPIWIIIFGVIFCIIVAIALLILSGIWQRRRNKEPSEVD 180
DB 121 QTLFELKIPSTLAPMDPSVPIWIIIFGVIFCIIVAIALLILSGIWQRRRNKEPSEVD 180
QY 181 DAEDKCNMTIENGIPSDPLDMKGGILMPS 212
DB 181 DAEDKCNMTIENGIPSDPLDMKGGILMPS 212

RESULT 2

AAB33447
ID AAB33447 standard; protein; 212 AA.

AC AAB33447;

XX 29-JAN-2001 (first entry)

DE Human PRO1312 protein UNQ678 SEQ ID NO:161.

XX Human; immune related disease; diagnosis; anti-inflammatory; cardiant;
KW dermatological; antiarthritic; antirheumatic; immunosuppressive;
KW haemostatic; antithyroid; antidiabetic; nootropic; neuroprotective;
KW antianaemic; hepatotropic; virucide; antipsoriatic; antiallergic;
KW antiasthmatic; systemic lupus erythematosus; rheumatoid arthritis;
KW osteoarthritis; spondyloarthropathy; systemic sclerosis; sarcoidosis;
KW idiopathic inflammatory myopathy; Sjogren's syndrome; thyroiditis;
KW systemic vasculitis; autoimmune haemolytic anaemia; diabetes mellitus;
KW autoimmune thrombocytopaenia; immune-mediated renal disease;
KW demyelinating disease; hepatobiliary disease; Whipple's disease;
KW inflammatory bowel disease; gluten-sensitive enteropathy;
KW autoimmune disease; immune-mediated skin disease; allergic disease;
KW immunological disease; transplantation associated disease;
KW graft rejection; graft-versus-host-disease.

XX Homo sapiens.

XX WO200053758-A2.

XX 14-SEP-2000.

PF 02-MAR-2000; 2000WO-US005841.

XX 08-MAR-1999; 99WO-US005028.
PR 10-MAR-1999; 99US-0123618P.
PR 12-MAR-1999; 99US-0123957P.
PR 23-MAR-1999; 99US-0125775P.
PR 12-APR-1999; 99US-0128849P.
PR 20-APR-1999; 99WO-US008615.
PR 28-APR-1999; 99US-0131445P.
PR 04-MAY-1999; 99US-0132371P.
PR 14-MAY-1999; 99US-0134287P.
PR 02-JUN-1999; 99WO-US012252.
PR 23-JUN-1999; 99US-0141037P.
PR 20-JUL-1999; 99US-0144758P.
PR 26-JUL-1999; 99US-0145698P.
PR 28-JUL-1999; 99US-0146222P.
PR 01-SEP-1999; 99WO-US020111.
PR 08-SEP-1999; 99WO-US020594.
PR 13-SEP-1999; 99WO-US020944.
PR 29-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 05-OCT-1999; 99WO-US023089.
PR 29-OCT-1999; 99US-0162506P.
PR 29-NOV-1999; 99WO-US028214.
PR 30-NOV-1999; 99WO-US028313.
PR 30-NOV-1999; 99WO-US028409.
PR 01-DEC-1999; 99WO-US028301.
PR 01-DEC-1999; 99WO-US028634.

PR 02-DEC-1999; 99WO-US028551.
PR 02-DEC-1999; 99WO-US028564.
PR 02-DEC-1999; 99WO-US028565.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030999.
PR 30-DEC-1999; 99WO-US031274.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000277.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 18-FEB-2000; 2000WO-US004342.
PR 22-FEB-2000; 2000WO-US004414.

(GETH) GENENTECH INC.

PI Ashkenazi AJ, Baker KP, Goddard A, Gurney AL, Hebert C, Henzel W;
PI Kabakoff RC, Lu Y, Pan J, Pennica D, Shelton DL, Smith V;
PI Stewart TA, Tumas D, Watanabe CK, Wood WI, Yan M;

DR WPI; 2000-572271/53.
DR N-PSDB; AAC58612.

PT Sixty four PRO polypeptides, useful in the diagnosis and treatment of
PT immune related disorders, e.g. systemic lupus erythematosus, rheumatoid
PT arthritis, osteoarthritis, thyroiditis and diabetes mellitus.

PS Claim 33; Fig 68; 309pp; English.

XX The present invention describes sixty four human PRO proteins which can
CC be used in the treatment of immune related diseases. The human PRO
CC proteins, anti-PRO antibodies, agonists and antagonists are useful for
CC treating and diagnosing immune related disorders. The disorders are
CC selected from systemic lupus erythematosus, rheumatoid arthritis,
CC osteoarthritis, juvenile chronic arthritis, spondyloarthropathies,
CC systemic sclerosis, idiopathic inflammatory myopathies, Sjogren's
CC syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic
CC anaemia, autoimmune thrombocytopaenia, thyroiditis, diabetes mellitus,
CC immune-mediated renal disease, demyelinating diseases of the central and
CC peripheral nervous systems, hepatobiliary diseases, inflammatory bowel
CC disease, gluten-sensitive enteropathy and Whipple's disease, autoimmune
CC or immune-mediated skin diseases, allergic diseases, immunological
CC diseases of the lung, and transplantation associated diseases including
CC graft rejection and graft-versus-host-disease. AAC58397 to AAC58578
CC represent PCR primers and hybridisation probes used in the isolation of
CC human PRO sequences. AAC58579 to AAC58642 and AAB33414 to AAB33477
CC represent human PRO polynucleotide and protein sequences given in the
CC exemplification of the present invention

XX SQ Sequence 212 AA;

Query Match 100.0%; Score 1102; DB 3; Length 212;
Best Local Similarity 100.0%; Pred. No. 5.8e-114;
Matches 212; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLWLLFFLVTAIHAELCQPGAENAFKVRISIRTAIGDKAYAWDTNVEYLFKAMVAFSMRK 60
Db 1 MLWLLFFLVTAIHAELCQPGAENAFKVRISIRTAIGDKAYAWDTNVEYLFKAMVAFSMRK 60
Qy 61 VNREATEISHVLLCNVTQVSFWFVVTDPKNTLPAVEVQSAIRMNKNRINNAPFLND 120
Db 61 VNREATEISHVLLCNVTQVSFWFVVTDPKNTLPAVEVQSAIRMNKNRINNAPFLND 120
Qy 121 QTLFELKIPSTLAPMDPSVPIWIIIFGVIFCIIVAIALLILSGIWQRRRNKEPSEVD 180
Db 121 QTLFELKIPSTLAPMDPSVPIWIIIFGVIFCIIVAIALLILSGIWQRRRNKEPSEVD 180
Qy 181 DAEDKCNMTIENGIPSDPLDMKGGILMPS 212
Db 181 DAEDKCNMTIENGIPSDPLDMKGGILMPS 212

RESULT 3

AAB24430
ID AAB24430 standard; protein; 212 AA.
XX
AC AAB24430;
XX
DT 07-NOV-2000 (first entry)
XX
DE Human PRO1312 protein sequence SEQ ID NO:214.
XX
XX Human; PRO; promotion; inhibition; angiogenesis; cardiovascularisation;
KW diagnosis; trauma; wound; cancer; atherosclerosis; cardiac hypertrophy;
KW angiogenic; proliferative; cardiac; cardiovascular; antiatherosclerotic;
KW cytotostatic; gene therapy; vaccine.
XX
OS Homo sapiens.
XX
PN WO200032221-A2.
XX
PD 08-JUN-2000.
XX
PP 30-NOV-1999; 99WO-US028313.
XX
PR 01-DEC-1998; 98WO-US025108.
PR 16-DEC-1998; 98US-0112850P.
PR 12-JAN-1999; 99US-0115554P.
PR 08-MAR-1999; 99WO-US005028.
PR 12-MAR-1999; 99US-0123957P.
PR 28-APR-1999; 99US-0131445P.
PR 14-MAY-1999; 99US-0134287P.
PR 02-JUN-1999; 99WO-US012252.
PR 23-JUN-1999; 99US-0141037P.
PR 20-JUL-1999; 99US-0144758P.
PR 26-JUL-1999; 99US-0145698P.
PR 01-SEP-1999; 99WO-US020111.
PR 08-SEP-1999; 99WO-US020594.
PR 13-SEP-1999; 99WO-US020944.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 05-OCT-1999; 99WO-US023089.
PR 29-OCT-1999; 99US-0162506P.
XX
PA (GETH) GENENTECH INC.
XX
PI Ashkenazi AJ, Baker KP, Ferrara N, Gerber H, Hillan KJ;
PI Goddard A, Godowski PJ, Gurney AL, Klein RD, Kuo SS, Paoni NF;
PI Smith V, Watanabe CK, Williams PM, Wood WI;
XX
DR WPI; 2000-412154/35.
DR N-PSDB; AAA77680.
XX
PT Nucleic acids encoding PRO polypeptides useful for preventing, diagnosing
PT and treating diagnosing a cardiovascular, endothelial or angiogenic
PT disorders in mammals.
XX
PS Claim 72; Fig 86; 315pp; English.
XX
CC The present invention describes nucleic acids encoding PRO polypeptides
CC useful for preventing, diagnosing and treating diagnosing a
CC cardiovascular, endothelial or angiogenic disorder in mammals by
CC modulating cell proliferation, angiogenesis and cardiovascularisation,
CC and for identifying agonists and antagonists of these processes. The
CC nucleic acids and the proteins they encode may be used in the prevention,
CC treatment and diagnosis of diseases associated with inappropriate PRO
CC expression such as cardiovascular, endothelial or angiogenic disorders in
CC mammals (e.g. atherosclerosis, cancers and cardiac hypertrophy). For
CC example, the nucleic acids (NCs) and vectors containing them and the PRO
CC polypeptide may be used to treat disorders associated with decreased PRO
CC expression. AAA77510 to AAA77721 and AAB24388 to AAB24435 represent
CC nucleotide and protein sequences used in the exemplification of the
CC present invention
XX
SQ Sequence 212 AA;

Query Match 100.0%; Score 1102; DB 3; Length 212;
Best Local Similarity 100.0%; Pred. No. 5.8e-114;
Matches 212; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLWLLFELVTAIHAEICQPGAENAFKVRLLSIRTALGDKAYAWDTNEEYLFKAMVAFSMRK 60
DB 1 MLWLLFELVTAIHAEICQPGAENAFKVRLLSIRTALGDKAYAWDTNEEYLFKAMVAFSMRK 60
QY 61 VPRNREATEISHVLLCNVTQVSFVFVTDPSKNHTLPAVEVQSAIRMNKNRINNAPFLND 120
DB 61 VPRNREATEISHVLLCNVTQVSFVFVTDPSKNHTLPAVEVQSAIRMNKNRINNAPFLND 120
QY 121 QTLEFLKIPSTLAPPMDPSVPIWIIIFGVIFCIIIVAIALLILSGIWQRRRNKKEPSEVD 180
DB 121 QTLEFLKIPSTLAPPMDPSVPIWIIIFGVIFCIIIVAIALLILSGIWQRRRNKKEPSEVD 180
QY 181 DAEDKCNMTITIENGIPSDPLDMKGGILMMP 212
DB 181 DAEDKCNMTITIENGIPSDPLDMKGGILMMP 212
RESULT 4
AAU12412
ID AAU12412 standard; protein; 212 AA.
XX
AC AAU12412;
XX
DT 24-OCT-2001 (first entry)
XX
DE Human PRO1312 polypeptide sequence.
XX
KW Human secretory and transmembrane; PRO; mammalian; cancer; lung; breast;
KW prostate; cervical; tumour necrosis factor-alpha; TNF-alpha; cartilage;
KW ear; proliferation; glucose; free fatty acid; skeletal muscle; adipocyte;
KW A-peptide; factor VIIA; gene therapy.
XX
OS Homo sapiens.
XX
PN WO200140466-A2.
XX
PD 07-JUN-2001.
XX
PP 01-DEC-2000; 2000WO-US032678.
XX
PR 01-DEC-1999; 99WO-US028301.
PR 01-DEC-1999; 99WO-US028634.
PR 02-DEC-1999; 99WO-US028551.
PR 02-DEC-1999; 99WO-US028564.
PR 02-DEC-1999; 99WO-US028565.
PR 09-DEC-1999; 99US-0170262P.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 20-DEC-1999; 99WO-US030999.
PR 30-DEC-1999; 99WO-US031243.
PR 30-DEC-1999; 99WO-US031274.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000277.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 18-FEB-2000; 2000WO-US004342.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US004914.
PR 24-FEB-2000; 2000WO-US005004.
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005841.
PR 03-MAR-2000; 2000US-0187202P.
PR 10-MAR-2000; 2000WO-US006319.
PR 15-MAR-2000; 2000WO-US006884.
PR 20-MAR-2000; 2000WO-US007377.
PR 21-MAR-2000; 2000WO-US007532.
PR 30-MAR-2000; 2000WO-US008439.
PR 17-MAY-2000; 2000WO-US013705.

PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 05-JUN-2000; 2000US-0209832P.
PR 28-JUL-2000; 2000WO-US020710.
PR 11-AUG-2000; 2000WO-US022031.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000WO-US030952.
PR 10-NOV-2000; 2000WO-US030873.
XX
PA (GETH) GENENTECH INC.
XX
PI Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;
PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
XX
DR WPI; 2001-408281/43.
DR N-PSDB; AAS21484.
XX
PT Isolated , secretory and transmembrane PRO polypeptide used to detect
PT other PRO polypeptides, link bioactive molecules to cells expressing PRO
PT polypeptides, and detect the presence of mammalian tumors e.g. lung,
PT breast, prostate, cervical.
XX
PS Claim 12; Fig 482; 813pp; English.
XX
CC AAU12172-AAU12446 represent novel human secretory and transmembrane PRO
CC polypeptides. The PRO polypeptides are useful to detect other PRO
CC polypeptides, to link bioactive molecules to cells expressing PRO
CC polypeptides, to modulate biological activities of cells expressing PRO
CC polypeptides, and to detect the presence of mammalian lung, colon,
CC breast, prostate, rectal, cervical or liver tumours by comparing PRO
CC polypeptide expression in a cell sample to that in a control sample. Some
CC of the 275 sequences are also useful to stimulate the release of tumour
CC necrosis factor-alpha (TNF-alpha) from human blood, the proliferation or
CC differentiation of chondrocytes, the proliferation or gene expression in
CC pericyte cells, the release of proteoglycans from cartilage, the
CC proliferation of inner ear utricular supporting cells or of T-
CC lymphocytes, the release of a cytokine from peripheral blood monocytes
CC (PBMCs), or the proliferation of endothelial cells. Some of the PRO
CC polypeptides may modulate glucose or free fatty acid uptake by skeletal
CC muscle cells or by adipocytes; or inhibit binding of A-peptide to factor
CC VIIA. The PRO polypeptides can be used in assays to identify molecules
CC involved in binding interactions. The polynucleotides encoding PRO
CC polypeptides can be used to generate probes, antisense RNA/DNA,
CC transgenic or knock out animals and can be used in gene therapy
XX
SQ Sequence 212 AA;
Query Match 100.0%; Score 1102; DB 4; Length 212;
Best Local Similarity 100.0%; Pred. No. 5.8e-114;
Matches 212; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MLWLLFVLTAIHAEICQPGAEAFKVRLLSIRLTALGDKAYAWDTNVEYLFKAMVAFSMRK 60
Db 1 MLWLLFVLTAIHAEICQPGAEAFKVRLLSIRLTALGDKAYAWDTNVEYLFKAMVAFSMRK 60
Qy 61 VFNREATEISHVLLCNVTQVSFVVTDPSPKNTLPAVEVQSAIRMNKNRINNAPFLND 120
Db 61 VFNREATEISHVLLCNVTQVSFVVTDPSPKNTLPAVEVQSAIRMNKNRINNAPFLND 120
Qy 121 QTLFELKIPSTLAPMDPSVPIWIIIFGVIFCIIVAIALLILSGIWQRRRKNKEPSEVD 180
Db 121 QTLFELKIPSTLAPMDPSVPIWIIIFGVIFCIIVAIALLILSGIWQRRRKNKEPSEVD 180
Qy 181 DAEDKCNMITIENGIPSDPLDMKGILMPS 212
Db 181 DAEDKCNMITIENGIPSDPLDMKGILMPS 212
RESULT 5
AAB65274

ID AAB65274 standard; protein; 212 AA.
XX
AC AAB65274;
XX
DT 02-APR-2001 (first entry)
XX
DE Human PRO1312 (UNQ678) protein sequence SEQ ID NO:387.
XX
KW Human; secreted and transmembrane protein; PRO; cytostatic; cell death;
KW cancer; chromosomal mapping; gene mapping; tissue typing;
KW diagnostic assay.
XX
OS Homo sapiens.
XX
PN WO200073454-A1.
XX
PD 07-DEC-2000.
XX
PF 30-MAR-2000; 2000WO-US008439.
XX
PR 02-JUN-1999; 99WO-US012252.
PR 23-JUN-1999; 99US-0141037P.
PR 07-JUL-1999; 99US-0143048P.
PR 20-JUL-1999; 99US-0144758P.
PR 26-JUL-1999; 99US-0145698P.
PR 28-JUL-1999; 99US-0146222P.
PR 17-AUG-1999; 99US-0149396P.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 08-OCT-1999; 99US-0158663P.
PR 30-NOV-1999; 99WO-US028313.
PR 01-DEC-1999; 99WO-US028301.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US004914.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 15-MAR-2000; 2000WO-US006884.
PR 20-MAR-2000; 2000WO-US007377.
XX
PA (GETH) GENENTECH INC.
XX
PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
PI Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi CJ, Gurney AL, Kljavin IJ, Napier MA, Pan J, Paoni NF;
PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;
PI Zhang Z;
XX
DR WPI; 2001-032160/04.
DR N-PSDB; AAF44243.
XX
PT PRO polynucleotides used to produce polypeptides used to target bioactive
PT molecules such as toxins, radiolabels or antibodies, to specific cells,
PT to cause targeted cell death.
XX
PS Claim 12; Fig 278; 935pp; English.
XX
CC The present invention describes human secreted and transmembrane PRO
CC proteins. The PRO proteins have cytostatic activity. The PRO proteins can
CC be used for targeted delivery of bioactive molecules, such as toxins,
CC radiolabels or antibodies, that cause cell death. PRO nucleotide
CC sequences, and their fragments, can be used as hybridisation probes, in
CC chromosomal and gene mapping, and in the generation of anti-sense RNA and
CC DNA. They may also be used to produce transgenic animals which are used
CC to develop and screen therapeutically useful reagents. The PRO nucleotide
CC and protein sequence can be used for tissue typing and in treating
CC cancer. Anti-PRO antibodies can be used in diagnostic assays. AAF44270 to
CC AAF44470 represent PCR primers and hybridisation probes used in the

```
CC isolation of human PRO sequences. AAF44087 to AAF44269 and AAB65154 to
CC AAB65300 represent human PRO polynucleotide and protein sequences given
CC in the exemplification of the present invention
XX
SQ Sequence 212 AA;

Query Match 100.0%; Score 1102; DB 4; Length 212;
Best Local Similarity 100.0%; Pred. No. 5.8e-114;
Matches 212; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLWLLFFLVTAIHAEIQCQGAENAFKVRISIRIALGDKAYAWDTNEEYLFKAMVAFSMRK 60
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Db 1 MLWLLFFLVTAIHAEIQCQGAENAFKVRISIRIALGDKAYAWDTNEEYLFKAMVAFSMRK 60

QY 61 VFNREATEISHVLLCNVTQRVSFVVTDPKSNHTLPAVEVQSAIRMNKNRINNAPFLND 120
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Db 61 VFNREATEISHVLLCNVTQRVSFVVTDPKSNHTLPAVEVQSAIRMNKNRINNAPFLND 120

QY 121 QTLFELKIPSTLAPMDPSVPIWIIIFGVIFCIIIVAIALLILSGIWQRRRKNKEPSEVD 180
   |||||
Db 121 QTLFELKIPSTLAPMDPSVPIWIIIFGVIFCIIIVAIALLILSGIWQRRRKNKEPSEVD 180

QY 181 DAEDKCNMITIENGIPSDPLDMKGGILMMP 212
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Db 181 DAEDKCNMITIENGIPSDPLDMKGGILMMP 212

RESULT 6
ABU58089
ID ABU58089 standard; protein; 212 AA.
XX
AC ABU58089;
XX
DT 14-APR-2003 (first entry)
XX
DE Human PRO polypeptide #121.
XX
KW Human; PRO; cytostatic; tumour; cancer; breast; lung; stomach; liver;
KW horse; cow; dog; cat; sheep; pig; goat; rabbit; ADEPT;
KW antibody-dependent enzyme mediated prodrug therapy.
XX
OS Homo sapiens.
XX
PN US2003027163-A1.
XX
PD 06-FEB-2003.
XX
PF 15-NOV-2001; 2001US-00997666.
XX
PR 16-JUN-1997; 97US-0049787P.
PR 17-OCT-1997; 97US-0062250P.
PR 05-NOV-1997; 97WO-US020069.
PR 12-NOV-1997; 97US-0065186P.
PR 13-NOV-1997; 97US-0065311P.
PR 24-NOV-1997; 97US-0066770P.
PR 25-FEB-1998; 98US-0075945P.
PR 20-MAR-1998; 98US-0078910P.
PR 28-APR-1998; 98US-0083322P.
PR 07-MAY-1998; 98US-0084600P.
PR 28-MAY-1998; 98US-0087106P.
PR 02-JUN-1998; 98US-0087607P.
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PR 02-JUN-1998; 98US-0087759P.
PR 03-JUN-1998; 98US-0087827P.
PR 04-JUN-1998; 98US-0088021P.
PR 04-JUN-1998; 98US-0088025P.
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PR 04-JUN-1998; 98US-0088326P.
PR 05-JUN-1998; 98US-0088167P.
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PR 05-JUN-1998; 98US-0088202P.
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PR 09-JUN-1998; 98US-0088655P.
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PR 16-JUN-1998; 98US-0089512P.
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PR 10-JUL-1998; 98US-0092472P.
PR 30-JUL-1998; 98US-0093339P.
PR 04-AUG-1998; 98US-0094651P.
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PR 04-AUG-1998; 98US-0095302P.
PR 04-AUG-1998; 98US-0095318P.
PR 04-AUG-1998; 98US-0095321P.
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PR 04-AUG-1998; 98US-0095325P.
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PR 10-AUG-1998; 98US-0095929P.
PR 10-AUG-1998; 98US-0096012P.
PR 11-AUG-1998; 98US-0096143P.
PR 11-AUG-1998; 98US-0096146P.
PR 12-AUG-1998; 98US-0096329P.
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PR 18-AUG-1998; 98US-0097022P.
PR 19-AUG-1998; 98US-0097141P.
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PR 26-AUG-1998; 98US-0097952P.
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PR 26-AUG-1998; 98US-0097971P.
PR 26-AUG-1998; 98US-0097974P.
PR 26-AUG-1998; 98US-0097978P.
PR 26-AUG-1998; 98US-0097979P.
PR 26-AUG-1998; 98US-0097986P.
PR 31-AUG-1998; 98US-0098014P.
PR 16-SEP-1998; 98US-0098525P.
PR 16-SEP-1998; 98US-0100634P.
PR 16-SEP-1998; 98US-0100858P.
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PR 17-SEP-1998; 98US-0101943P.
PR 07-OCT-1998; 98US-0102114P.
PR 01-DEC-1998; 98US-01025108.
PR 22-DEC-1998; 98US-0113296P.
PR 05-JAN-1999; 98US-01000106.
PR 08-MAR-1999; 98US-01005028.
PR 12-MAR-1999; 98US-0123957P.
PR 02-JUN-1999; 98US-0123957P.
PR 23-JUN-1999; 98US-0141037P.
PR 07-JUL-1999; 98US-0143048P.
PR 20-JUL-1999; 98US-0144758P.
PR 26-JUL-1999; 98US-0145698P.
PR 28-JUL-1999; 98US-0146222P.
PR 17-AUG-1999; 98US-0149396P.
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PR 15-SEP-1999; 98US-015021090.
PR 15-SEP-1999; 98US-015021547.
PR 08-OCT-1999; 98US-0158663P.
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PR 01-DEC-1999; 98US-0158663P.
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PR 20-DEC-1999; 98US-0158663P.
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PR 06-JAN-2000; 98US-0158663P.
PR 11-FEB-2000; 98US-0158663P.
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PR 24-FEB-2000; 98US-0158663P.
PR 02-MAR-2000; 98US-0158663P.
PR 10-MAR-2000; 98US-0158663P.
PR 15-MAR-2000; 98US-0158663P.
PR 20-MAR-2000; 98US-0158663P.
PR 30-MAR-2000; 98US-0158663P.
PR 15-MAY-2000; 98US-0158663P.

PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 23-JUN-2000; 2000US-0213637P.
PR 28-JUL-2000; 2000WO-US020710.
PR 11-AUG-2000; 2000WO-US022031.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 07-SEP-2000; 2000US-0230978P.

Query Match 100.0%; Score 1102; DB 6; Length 212;
Best Local Similarity 100.0%; Pred. No. 5.8e-114;
Matches 212; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLWLLPFLVTAIHAELCQPGAENAFKVRLSIRTAIGDKAYAWDTNEEYLFKAMVAFSMRK 60
Db 1 MLWLLPFLVTAIHAELCQPGAENAFKVRLSIRTAIGDKAYAWDTNEEYLFKAMVAFSMRK 60

Qy 61 VPREATEISHVLLCNVTQVSFWFVVTDPKSNHTLPAVEVQSAIRMNKRNINNAFLND 120
Db 61 VPREATEISHVLLCNVTQVSFWFVVTDPKSNHTLPAVEVQSAIRMNKRNINNAFLND 120

Qy 121 QTLFLKIPSTLAPMDPSVPIIIFGVIFCIIVAIALLILSGIWQRRRKKEPSEVD 180
Db 121 QTLFLKIPSTLAPMDPSVPIIIFGVIFCIIVAIALLILSGIWQRRRKKEPSEVD 180

Qy 181 DAEDKCNMTIENGIPSDPLDMKGGILMMP 212
Db 181 DAEDKCNMTIENGIPSDPLDMKGGILMMP 212

RESULT 7
ABUS9167
ID ABUS9167 standard; protein; 212 AA.
XX ABUS9167;
AC ABUS9167;
XX 28-APR-2003 (first entry)
XX Novel human secreted or transmembrane protein PRO1312.
DE Human; PRO; hypertrophy of neonatal heart; angiogenesis; wound healing;
KW cardiac insufficiency disorder; cancer; tumour; immune response;
KW adrenal cortical capillary endothelial growth; c-fos induction;
KW vascular endothelial growth factor inhibition; VEGF inhibition;
KW endothelial cell growth inhibitor; T-lymphocytes stimulation;
KW retinal neurons cell survival; rod photoreceptor cell survival;
KW retinal disorder; retinitis pigmentosa; kidney disorder;
KW mammalian kidney mesangial cell proliferation; Berger disease;
KW dermatitis; herpeticiformis; Crohn's disease; chondrocyte proliferation;
KW chondrocyte redifferentiation; sports injury; arthritis.

XX Homo sapiens.
OS US2002132252-A1.
XX 19-SEP-2002.
XX 14-NOV-2001; 2001US-00990442.
XX 16-JUN-1997; 97US-0049787P.
PR 17-OCT-1997; 97US-0062250P.
PR 05-NOV-1997; 97WO-US020069.
PR 12-NOV-1997; 97US-0065186P.
PR 13-NOV-1997; 97US-0065311P.
PR 24-NOV-1997; 97US-0066770P.
PR 25-FEB-1998; 98US-0075945P.
PR 20-MAR-1998; 98US-0078910P.
PR 28-APR-1998; 98US-0083322P.
PR 07-MAY-1998; 98US-0084600P.
PR 28-MAY-1998; 98US-0087106P.
PR 02-JUN-1998; 98US-0087607P.

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PR 03-JUN-1998; 98US-0087827P.
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PR 18-JUN-1998; 98US-0089801P.
PR 18-JUN-1998; 98US-0089907P.
PR 18-JUN-1998; 98US-0089908P.
PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98WO-US019437.
PR 07-OCT-1998; 98WO-US021141.
PR 01-DEC-1998; 98WO-US025108.
PR 05-JAN-1999; 99WO-US000106.
PR 08-MAR-1999; 99WO-US005028.
PR 02-JUN-1999; 99WO-US012252.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 30-NOV-1999; 99WO-US028313.
PR 01-DEC-1999; 99WO-US028301.
PR 01-DEC-1999; 99WO-US028634.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 06-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US004914.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 10-MAR-2000; 2000WO-US006319.
PR 15-MAR-2000; 2000WO-US006884.
PR 20-MAR-2000; 2000WO-US007377.
PR 30-MAR-2000; 2000WO-US008439.
PR 15-MAY-2000; 2000WO-US013358.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 11-AUG-2000; 2000WO-US022031.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.

PR 08-NOV-2000; 2000WO-US030952.
PR 01-DEC-2000; 2000WO-US032678.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-JUN-2001; 2001WO-US017800.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 28-AUG-2001; 2001US-00941992.
XX
PA (GETH) GENENTECH INC.
XX
XX
PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
PI Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi JC, Gurney AL, Kljavin IJ, Napier MA, Pan J, Paoni NF;
PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;
PI Zhang Z;
XX
XX WPI; 2003-247083/24.
DR N-PSDB; ABX80370.
DR
XX
PT Novel isolated PRO polypeptides e.g., PRO826, PRO1068, PRO1184, PRO1346
PT and PRO1375, which stimulate proliferation of stimulated T-lymphocytes
PT are therapeutically useful for enhancing immune response and in cancer
PT treatments.
XX
PS Claim 12; Fig 278; 648pp; English.
XX
CC The invention describes an isolated human PRO polypeptide. The PRO
CC polypeptides are useful in detecting PRO polypeptides in a sample, in
CC linking a bioactive molecule to a cell expressing a PRO polypeptide, and
CC in modulating at least one biological activity of a cell expressing a PRO
CC polypeptide. PRO1312 stimulates hypertrophy of neonatal heart and is thus
CC useful for treating cardiac insufficiency disorders. PRO1154 and PRO1186
CC stimulate adrenal cortical capillary endothelial growth, and PRO536,
CC PRO943, PRO828, PRO826, PRO1068 or PRO535, PRO826, PRO819, PRO1126,
CC PRO1360 and PRO1387 induce c-fos in endothelial cells, and are thus
CC useful for treating conditions or disorders where angiogenesis would be
CC beneficial, e.g. wound healing and antagonist of this polypeptide are
CC useful for treating cancerous tumours. PRO812 inhibits vascular
CC endothelial growth factor (VEGF) stimulated proliferation of endothelial
CC cells and is thus useful for inhibiting endothelial cell growth in
CC mammals which would be beneficial in inhibiting tumour growth. PRO826,
CC PRO1068, PRO1184, PRO1346 and PRO1375 stimulate proliferation of
CC stimulated T-lymphocytes and are therapeutically useful for enhancing
CC immune response. PRO828, PRO826, PRO1068 or PRO1132 enhance survival of
CC retinal neurons cells (PRO1132 is also enhances survival/proliferation of
CC rod photoreceptor cells) and therefore are useful for treating retinal
CC disorders of injuries, e.g. retinitis pigmentosa, AMD. PRO819, PRO813
CC and PRO11066 induce proliferation of mammalian kidney mesangial cells,
CC and therefore are useful for treating kidney disorders associated with
CC decreased mesangial cell function such as Berger disease or other
CC nephropathies associated with dermatitis, herpeticiformis or Crohn's
CC disease. PRO1310, PRO844, PRO1312, PRO1192 and PRO1387 induce the
CC proliferation and/or redifferentiation of chondrocytes in culture and are
CC thus useful for treating sports injuries, and arthritis. This is the
CC amino acid sequence of a novel human PRO protein
XX
SQ Sequence 212 AA;

Query Match 100.0%; Score 1102; DB 6; Length 212;
Best Local Similarity 100.0%; Pred. No. 5.8e-114;
Matches 212; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLWLLFFLVTAIHAELCQGAENAFKVLRSIRLTALGDKAYAWDTNEEYLFKAMVAFSMRK 60
Db 1 MLWLLFFLVTAIHAELCQGAENAFKVLRSIRLTALGDKAYAWDTNEEYLFKAMVAFSMRK 60

Qy 61 VPNREATEISHVLLCNVTQVSFWFVTDPSKNHTLPAVEVQSAIRMNKRINNAFFLND 120
Db 61 VPNREATEISHVLLCNVTQVSFWFVTDPSKNHTLPAVEVQSAIRMNKRINNAFFLND 120

Qy 121 QTLFLKIPSTLAPMDPSVPIWIIIFGVIFCIIIVAIALLISGIWQRRRNKEPSEVD 180
Db 121 QTLFLKIPSTLAPMDPSVPIWIIIFGVIFCIIIVAIALLISGIWQRRRNKEPSEVD 180

Db 121 QTLEFLKIPSTLAPPMDPSVPINIIIFGVIFCIIVAIALLILSGIWQRRRKNKEPSEVD 180
QY 181 DAEDKCENMITIENGIPSDPLDMKGGILMPS 212
Db 181 DAEDKCENMITIENGIPSDPLDMKGGILMPS 212
RESULT 8
ID ABU82679 standard; protein; 212 AA.
XX ABU82679;
AC
XX
DT 26-JUN-2003 (first entry)
XX
DE Human secreted/transmembrane protein PRO1312.
XX
KW Human; PRO; secreted protein; transmembrane protein;
KW cardiac insufficiency disorders; angiogenesis; wound healing;
KW cancerous tumour; immune response; retinal disorder; sight loss;
KW retinitis pigmentosum; age-related macular degeneration; AMD;
KW kidney disorder; Berger disease; nephropathy; dermatitis; herpetiformis;
KW Crohn's disease; sports injury; arthritis.
XX
OS Homo sapiens.
XX
PN US2003032023-A1.
XX
PD 13-FEB-2003.
XX
PF 14-NOV-2001; 2001US-00990711.
XX
PR 16-JUN-1997; 97US-0049787P.
PR 17-OCT-1997; 97US-0062250P.
PR 05-NOV-1997; 97WO-US020069.
PR 12-NOV-1997; 97US-0065186P.
PR 13-NOV-1997; 97US-0065311P.
PR 24-NOV-1997; 97US-0066770P.
PR 25-FEB-1998; 98US-0075945P.
PR 20-MAR-1998; 98US-0078910P.
PR 28-APR-1998; 98US-0083322P.
PR 07-MAY-1998; 98US-0084600P.
PR 28-MAY-1998; 98US-0087106P.
PR 02-JUN-1998; 98US-0087607P.
PR 02-JUN-1998; 98US-0087609P.
PR 02-JUN-1998; 98US-0087759P.
PR 03-JUN-1998; 98US-0087827P.
PR 04-JUN-1998; 98US-0088021P.
PR 04-JUN-1998; 98US-0088025P.
PR 04-JUN-1998; 98US-0088026P.
PR 04-JUN-1998; 98US-0088028P.
PR 04-JUN-1998; 98US-0088029P.
PR 04-JUN-1998; 98US-0088030P.
PR 04-JUN-1998; 98US-0088033P.
PR 04-JUN-1998; 98US-0088326P.
PR 05-JUN-1998; 98US-0088167P.
PR 05-JUN-1998; 98US-0088202P.
PR 05-JUN-1998; 98US-0088212P.
PR 05-JUN-1998; 98US-0088217P.
PR 09-JUN-1998; 98US-0088655P.
PR 10-JUN-1998; 98US-0088734P.
PR 10-JUN-1998; 98US-0088738P.
PR 10-JUN-1998; 98US-0088742P.
PR 10-JUN-1998; 98US-0088810P.
PR 10-JUN-1998; 98US-0088824P.
PR 10-JUN-1998; 98US-0088826P.
PR 11-JUN-1998; 98US-0088858P.
PR 11-JUN-1998; 98US-0088861P.
PR 11-JUN-1998; 98US-0088876P.
PR 12-JUN-1998; 98US-0089105P.
PR 16-JUN-1998; 98US-0089440P.
PR 16-JUN-1998; 98US-0089512P.
PR 16-JUN-1998; 98US-0089514P.
PR 17-JUN-1998; 98US-0089532P.
PR 17-JUN-1998; 98US-0089538P.
PR 17-JUN-1998; 98US-0089598P.
PR 17-JUN-1998; 98US-0089599P.
PR 17-JUN-1998; 98US-0089600P.
PR 17-JUN-1998; 98US-0089653P.
PR 18-JUN-1998; 98US-0089801P.
PR 18-JUN-1998; 98US-0089907P.
PR 18-JUN-1998; 98US-0089908P.
PR 19-JUN-1998; 98US-0089947P.
PR 19-JUN-1998; 98US-0089948P.
PR 19-JUN-1998; 98US-0089952P.
PR 22-JUN-1998; 98US-0090246P.
PR 22-JUN-1998; 98US-0090252P.
PR 23-JUN-1998; 98US-0090349P.
PR 23-JUN-1998; 98US-0090355P.
PR 24-JUN-1998; 98US-0090429P.
PR 24-JUN-1998; 98US-0090431P.
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PR 24-JUN-1998; 98US-0090445P.
PR 24-JUN-1998; 98US-0090472P.
PR 24-JUN-1998; 98US-0090535P.
PR 24-JUN-1998; 98US-0090540P.
PR 24-JUN-1998; 98US-0090542P.
PR 24-JUN-1998; 98US-0090557P.
PR 25-JUN-1998; 98US-0090676P.
PR 25-JUN-1998; 98US-0090678P.
PR 25-JUN-1998; 98US-0090690P.
PR 25-JUN-1998; 98US-0090694P.
PR 25-JUN-1998; 98US-0090695P.
PR 25-JUN-1998; 98US-0090696P.
PR 26-JUN-1998; 98US-0090862P.
PR 01-JUL-1998; 98US-0090863P.
PR 01-JUL-1998; 98US-0091360P.
PR 01-JUL-1998; 98US-0091544P.
PR 02-JUL-1998; 98US-0091478P.
PR 02-JUL-1998; 98US-0091519P.
PR 02-JUL-1998; 98US-0091626P.
PR 02-JUL-1998; 98US-0091628P.
PR 02-JUL-1998; 98US-0091633P.
PR 02-JUL-1998; 98US-0091646P.
PR 02-JUL-1998; 98US-0091673P.
PR 07-JUL-1998; 98US-0091978P.
PR 07-JUL-1998; 98US-0091982P.
PR 09-JUL-1998; 98US-0092182P.
PR 10-JUL-1998; 98US-0092472P.
PR 20-JUL-1998; 98US-0093339P.
PR 30-JUL-1998; 98US-0094651P.
PR 04-AUG-1998; 98US-0095282P.
PR 04-AUG-1998; 98US-0095285P.
PR 04-AUG-1998; 98US-0095301P.
PR 04-AUG-1998; 98US-0095302P.
PR 04-AUG-1998; 98US-0095318P.
PR 04-AUG-1998; 98US-0095321P.
PR 04-AUG-1998; 98US-0095325P.
PR 10-AUG-1998; 98US-0095916P.
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PR 10-AUG-1998; 98US-0096012P.
PR 11-AUG-1998; 98US-0096143P.
PR 11-AUG-1998; 98US-0096146P.
PR 12-AUG-1998; 98US-0096329P.
PR 17-AUG-1998; 98US-0096757P.
PR 17-AUG-1998; 98US-0096766P.
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PR 17-AUG-1998; 98US-0096791P.
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PR 17-AUG-1998; 98US-0096894P.
PR 17-AUG-1998; 98US-0096895P.
PR 17-AUG-1998; 98US-0096897P.

PR 18-AUG-1998; 98US-0096949P.
PR 18-AUG-1998; 98US-0096950P.
PR 18-AUG-1998; 98US-0096959P.
PR 18-AUG-1998; 98US-0096960P.
PR 18-AUG-1998; 98US-0097022P.
PR 19-AUG-1998; 98US-0097141P.
PR 20-AUG-1998; 98US-0097218P.
PR 24-AUG-1998; 98US-0097661P.
PR 26-AUG-1998; 98US-0097952P.
PR 26-AUG-1998; 98US-0097954P.
PR 26-AUG-1998; 98US-0097955P.
PR 26-AUG-1998; 98US-0097971P.
PR 26-AUG-1998; 98US-0097974P.
PR 26-AUG-1998; 98US-0097978P.
PR 26-AUG-1998; 98US-0097979P.
PR 26-AUG-1998; 98US-0097986P.
PR 26-AUG-1998; 98US-0098014P.
PR 31-AUG-1998; 98US-0098525P.
PR 16-SEP-1998; 98US-0100634P.
PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98US-0100858P.
PR 17-SEP-1998; 98WO-US019437.
PR 07-OCT-1998; 98WO-US021141.
PR 01-DEC-1998; 98WO-US025108.
PR 22-DEC-1998; 98US-0113296P.
PR 05-JAN-1999; 99WO-US000106.
PR 08-MAR-1999; 99WO-US005028.
PR 12-MAR-1999; 99US-0123957P.
PR 02-JUN-1999; 99WO-US012252.
PR 23-JUN-1999; 99US-0141037P.
PR 07-JUL-1999; 99US-0143048P.
PR 20-JUL-1999; 99US-0144758P.
PR 26-JUL-1999; 99US-0145698P.
PR 28-JUL-1999; 99US-0146222P.
PR 17-AUG-1999; 99US-0149396P.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 08-OCT-1999; 99US-0158663P.
PR 30-NOV-1999; 99WO-US028313.
PR 01-DEC-1999; 99WO-US028301.
PR 16-DEC-1999; 99WO-US028634.
PR 20-DEC-1999; 99WO-US030911.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US004914.
PR 02-MAR-2000; 2000WO-US005841.
PR 10-MAR-2000; 2000WO-US006319.
PR 15-MAR-2000; 2000WO-US006884.
PR 20-MAR-2000; 2000WO-US007377.
PR 30-MAR-2000; 2000WO-US008439.
PR 15-MAY-2000; 2000WO-US013358.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 23-JUN-2000; 2000US-0213637P.
PR 28-JUL-2000; 2000WO-US020710.
PR 11-AUG-2000; 2000WO-US022031.

Query Match 100.0%; Score 1102; DB 6; Length 212;
Best Local Similarity 100.0%; Pred. No. 5.8e-114;
Matches 212; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLWLLFFLVTAIHAE LCPQGAENAFKVR LSI RTALGDKAYAWDTNEEYLFKAMVAFSMRK 60
Db 1 MLWLLFFLVTAIHAE LCPQGAENAFKVR LSI RTALGDKAYAWDTNEEYLFKAMVAFSMRK 60
QY 61 VPNREATISHVLLCNVTQVSFWFVVTDP SKNHTLPAVEVQSAIRMKNKRINNAFFLND 120

Db 61 VPNREATISHVLLCNVTQVSFWFVVTDP SKNHTLPAVEVQSAIRMKNKRINNAFFLND 120
QY 121 QTLEFLKIPSTLAPMDPSVPIWIIIFGVIFCIIIVAIALLILSGIWORRRKNKPSVD 180
Db 121 QTLEFLKIPSTLAPMDPSVPIWIIIFGVIFCIIIVAIALLILSGIWORRRKNKPSVD 180
QY 181 DAEDKCNMITIENGIPSDPLDMKGGILMPS 212
Db 181 DAEDKCNMITIENGIPSDPLDMKGGILMPS 212
RESULT 9
ABO17856
ID ABO17856 standard; protein; 212 AA.
XX
AC ABO17856;
XX
DT 26-AUG-2003 (first entry)
XX
DE Novel human secreted and transmembrane protein PRO1312.
KW Human; secreted and transmembrane protein; PRO; antiinflammatory;
KW antiarteriosclerotic; cardiant; anti-infertility; anti-HIV; cytostatic;
KW antidiabetic; gene therapy; tumour necrosis factor (TNF)-alpha release;
KW TNF-alpha release; cell proliferation; cell differentiation;
KW gene expression modulator; proteoglycan release; cytokine release;
KW tumour; inflammatory disease; organ failure; atherosclerosis;
KW cardiac injury; infertility; birth defect; premature aging; AIDS;
KW acquired immunodeficiency syndrome; cancer; diabetic complication;
KW chromosome mapping; gene mapping; pharmaceutical; diagnostic; biosensor;
KW bioreactor; tissue typing.
XX
OS Homo sapiens.
XX
XX
PN US2003032156-A1.
XX
PD 13-FEB-2003.
XX
PF 06-MAY-2002; 2002US-00140474.
XX
PR 31-MAR-1997; 97WO-US005230.
PR 12-JUN-1998; 98WO-US012456.
PR 14-JUL-1998; 98WO-US014552.
PR 28-AUG-1998; 98WO-US017888.
PR 10-SEP-1998; 98WO-US018824.
PR 14-SEP-1998; 98WO-US019093.
PR 14-SEP-1998; 98WO-US019094.
PR 14-SEP-1998; 98WO-US019177.
PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98WO-US019437.
PR 07-OCT-1998; 98WO-US021141.
PR 29-OCT-1998; 98WO-US022991.
PR 29-OCT-1998; 98WO-US022992.
PR 20-NOV-1998; 98WO-US024855.
PR 01-DEC-1998; 98WO-US025108.
PR 05-JAN-1999; 99WO-US000106.
PR 08-MAR-1999; 99WO-US005028.
PR 10-MAR-1999; 99WO-US005190.
PR 20-APR-1999; 99WO-US008615.
PR 14-MAY-1999; 99WO-US010733.
PR 02-JUN-1999; 99WO-US012252.
PR 01-SEP-1999; 99WO-US020111.
PR 08-SEP-1999; 99WO-US020594.
PR 13-SEP-1999; 99WO-US020944.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 05-OCT-1999; 99WO-US023089.
PR 29-NOV-1999; 99WO-US028214.
PR 30-NOV-1999; 99WO-US028313.
PR 30-NOV-1999; 99WO-US028409.
PR 01-DEC-1999; 99WO-US028301.
PR 01-DEC-1999; 99WO-US028634.

PR 02-DEC-1999; 99WO-US028551.
PR 02-DEC-1999; 99WO-US028564.
PR 02-DEC-1999; 99WO-US028565.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 20-DEC-1999; 99WO-US030999.
PR 22-DEC-1999; 99WO-US030720.
PR 30-DEC-1999; 99WO-US031243.
PR 30-DEC-1999; 99WO-US031274.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000277.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 18-FEB-2000; 2000WO-US004342.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US004914.
PR 24-FEB-2000; 2000WO-US005004.
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005746.
PR 02-MAR-2000; 2000WO-US005841.
PR 10-MAR-2000; 2000WO-US006319.
PR 15-MAR-2000; 2000WO-US006884.
PR 20-MAR-2000; 2000WO-US007377.
PR 21-MAR-2000; 2000WO-US007532.
PR 30-MAR-2000; 2000WO-US008439.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 11-AUG-2000; 2000WO-US022031.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000WO-US030952.
PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001US-00796498.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-MAR-2001; 2001WO-US006666.
PR 09-MAR-2001; 2001US-00802706.
PR 14-MAR-2001; 2001US-00808689.
PR 22-MAR-2001; 2001US-00816744.
PR 05-APR-2001; 2001US-00828366.
PR 10-MAY-2001; 2001US-00854208.
PR 18-MAY-2001; 2001US-00860216.
PR 25-MAY-2001; 2001US-00866028.
PR 25-MAY-2001; 2001US-00866034.
PR 25-MAY-2001; 2001WO-US017092.
PR 01-JUN-2001; 2001US-00872035.
PR 01-JUN-2001; 2001WO-US017800.
PR 05-JUN-2001; 2001US-00874503.
PR 14-JUN-2001; 2001US-00882636.
PR 19-JUN-2001; 2001US-00886342.
PR 20-JUN-2001; 2001WO-US019692.
PR 21-JUN-2001; 2001US-00887879.
PR 22-JUN-2001; 2001WO-US020116.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 18-JUL-2001; 2001US-00908827.
PR 06-AUG-2001; 2001US-00924419.
PR 09-AUG-2001; 2001US-00927796.
PR 16-AUG-2001; 2001US-00931836.
PR 19-DEC-2001; 2001US-00028072.

(GETH) GENENTECH INC.

PI Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff B, Gao W;
PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;

XX WPI; 2003-341980/32.
DR N-PSDB; ACD24093.
XX
PT New secreted and transmembrane PRO nucleic acids, for treating
PT inflammation, organ failure, atherosclerosis, cardiac injury,
PT infertility, birth defects, premature aging, acquired immunodeficiency
PT syndrome (AIDS), or cancer.
XX
PS Claim 12; Fig 482; 660pp; English.
XX
CC The invention describes an isolated nucleic acid (I) comprising, or which
CC has 80 % sequence identity to, or the full-length coding sequence of, one
CC of 275 nucleotide sequences, and which encodes a corresponding
CC polypeptide selected from 275 amino acid sequences, where all sequences
CC are given in the specification. The polypeptide encoded by (I) is used to
CC detect PRO polypeptides, link a bioactive molecule to a cell expressing a
CC PRO polypeptide, modulate a biological activity of a cell, stimulate the
CC release of tumour necrosis factor (TNF)-alpha from human blood, modulate
CC the uptake of glucose or free fatty acid by cells, stimulate or inhibit
CC the proliferation or differentiation of cells or gene expression,
CC stimulate the release of proteoglycans, stimulate the release of cytokine
CC from peripheral blood mononuclear cells, inhibit the binding of A-peptide
CC to factor VIIA, or detect the presence of tumour in a mammal. The nucleic
CC acid and polypeptide encoded by it, are useful for treating inflammatory
CC diseases, organ failure, atherosclerosis, cardiac injury, infertility,
CC birth defects, premature aging, acquired immunodeficiency syndrome
CC (AIDS), cancer, or diabetic complications. The nucleic acid is useful as
CC hybridisation probes, in chromosome and gene mapping, and in generating
CC antisense RNA or DNA. The polypeptides are useful as pharmaceuticals,
CC diagnostics, biosensors or bioreactors. Both are useful in tissue typing.
CC This is the amino acid sequence of a novel human secreted and
CC transmembrane PRO polypeptide
XX
SQ Sequence 212 AA;

Query Match 100.0%; Score 1102; DB 6; Length 212;
Best Local Similarity 100.0%; Pred. No. 5.8e-114;
Matches 212; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLWLLFFLVTAIHAELCOPGAENAFKVRLSIRITALGDKAYAWDTNTEYLKAMVAFSMRK 60
Db 1 MLWLLFFLVTAIHAELCOPGAENAFKVRLSIRITALGDKAYAWDTNTEYLKAMVAFSMRK 60
QY 61 VFNREATEISHVLLCNVTQVSFWFVTDPSKNHTLP AVEVQSAIRNNKRNINNAFFLND 120
Db 61 VFNREATEISHVLLCNVTQVSFWFVTDPSKNHTLP AVEVQSAIRNNKRNINNAFFLND 120
QY 121 QTLFLKIPSTLAPPMDSVPVWIIIFGVIFCIIVAIALLILSGIWQRRRNKKEPSEVD 180
Db 121 QTLFLKIPSTLAPPMDSVPVWIIIFGVIFCIIVAIALLILSGIWQRRRNKKEPSEVD 180
QY 181 DAEDKCENMITIENGIPSDPLDMKGGILMMPS 212
Db 181 DAEDKCENMITIENGIPSDPLDMKGGILMMPS 212

RESULT 10

ABU60598
ID ABU60598 standard; protein; 212 AA.

XX AC ABU60598;

XX DT 01-MAY-2003 (first entry)

XX DE Human secreted/transmembrane protein, #157.

XX KW Human; PRO; secreted; transmembrane; signal peptide; pharmaceutical;
XX diagnostic; therapeutic; gene therapy.

XX OS Homo sapiens.

XX PN US2002160384-A1.

XX 31-OCT-2002.
XX 14-NOV-2001; 2001US-00992598.
PR 16-JUN-1997; 97US-0049787P.
PR 17-OCT-1997; 97US-0062250P.
PR 05-NOV-1997; 97WO-US020069.
PR 12-NOV-1997; 97US-0065186P.
PR 13-NOV-1997; 97US-0065311P.
PR 24-NOV-1997; 97US-0066770P.
PR 25-FEB-1998; 98US-0075945P.
PR 20-MAR-1998; 98US-0078910P.
PR 28-APR-1998; 98US-0083322P.
PR 07-MAY-1998; 98US-0084600P.
PR 28-MAY-1998; 98US-0087106P.
PR 02-JUN-1998; 98US-0087607P.
PR 02-JUN-1998; 98US-0087759P.
PR 03-JUN-1998; 98US-0087827P.
PR 04-JUN-1998; 98US-0088021P.
PR 04-JUN-1998; 98US-0088025P.
PR 04-JUN-1998; 98US-0088026P.
PR 04-JUN-1998; 98US-0088028P.
PR 04-JUN-1998; 98US-0088029P.
PR 04-JUN-1998; 98US-0088030P.
PR 04-JUN-1998; 98US-0088033P.
PR 04-JUN-1998; 98US-0088326P.
PR 05-JUN-1998; 98US-0088167P.
PR 05-JUN-1998; 98US-0088202P.
PR 05-JUN-1998; 98US-0088212P.
PR 05-JUN-1998; 98US-0088217P.
PR 09-JUN-1998; 98US-0088655P.
PR 10-JUN-1998; 98US-0088734P.
PR 10-JUN-1998; 98US-0088738P.
PR 10-JUN-1998; 98US-0088742P.
PR 10-JUN-1998; 98US-0088810P.
PR 10-JUN-1998; 98US-0088824P.
PR 10-JUN-1998; 98US-0088826P.
PR 11-JUN-1998; 98US-0088858P.
PR 11-JUN-1998; 98US-0088861P.
PR 11-JUN-1998; 98US-0088876P.
PR 12-JUN-1998; 98US-0089105P.
PR 16-JUN-1998; 98US-0089440P.
PR 16-JUN-1998; 98US-0089512P.
PR 16-JUN-1998; 98US-0089514P.
PR 17-JUN-1998; 98US-0089532P.
PR 17-JUN-1998; 98US-0089538P.
PR 17-JUN-1998; 98US-0089598P.
PR 17-JUN-1998; 98US-0089599P.
PR 17-JUN-1998; 98US-0089600P.
PR 17-JUN-1998; 98US-0089653P.
PR 18-JUN-1998; 98US-0089801P.
PR 18-JUN-1998; 98US-0089907P.
PR 18-JUN-1998; 98US-0089908P.
PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98WO-US019437.
PR 07-OCT-1998; 98WO-US021141.
PR 01-DEC-1998; 98WO-US025108.
PR 05-JAN-1999; 99WO-US000106.
PR 08-MAR-1999; 99WO-US005028.
PR 02-JUN-1999; 99WO-US012252.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 30-NOV-1999; 99WO-US028313.
PR 01-DEC-1999; 99WO-US028301.
PR 01-DEC-1999; 99WO-US028634.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.

PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US004914.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 10-MAR-2000; 2000WO-US006319.
PR 15-MAR-2000; 2000WO-US006884.
PR 20-MAR-2000; 2000WO-US007377.
PR 30-MAR-2000; 2000WO-US008439.
PR 15-MAY-2000; 2000WO-US013358.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 11-AUG-2000; 2000WO-US022031.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000WO-US030952.
PR 01-DEC-2000; 2000WO-US032678.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-JUN-2001; 2001WO-US017800.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 28-AUG-2001; 2001US-00941992.

(GETH) GENENTECH INC.

PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
PI Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi JC, Gurney AL, Kljavin IJ, Napier MA, Pan J, Paoni NF;
PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;
PI Zhang Z;

XX WPI; 2003-288106/28.
DR N-PSDB; ABX90348.

XX New transmembrane polypeptides and nucleic acids encoding the
PT polypeptides, useful in gene therapy, in chromosome identification, as
PT chromosome markers, or in generating probes.

XX Claim 12; Fig 278; 650pp; English.

XX The invention discloses isolated PRO secreted/transmembrane polypeptides
CC comprising a sequence without signal peptide and the nucleic acid
CC encoding them. The polypeptides can be used to raise antibodies that
CC specifically bind to the PRO polypeptide, for linking a bioactive
CC molecule to a cell expressing a PRO protein and for modulating at least
CC one biological activity of a cell. The PRO polypeptides or
CC polynucleotides are also useful in gene therapy, in chromosome
CC identification, as chromosome markers, or in generating probes. The PRO
CC polypeptides are useful as molecular markers for protein electrophoresis,
CC and the isolated nucleic acids may be used for recombinantly expressing
CC those markers. The PRO polypeptides and nucleic acids may also be used in
CC tissue typing. Anti-PRO antibodies are useful in diagnostic assays for
CC PRO, and in affinity purification of PRO from recombinant cell culture or
CC natural sources. The sequences presented in ABU60478-ABU60624 are the PRO
CC polynucleotides of the invention. Note: The sequence data for this patent
CC is also available in electronic format from USPTO at
XX seqdata.uspto.gov/sequence.html

SQ Sequence 212 AA;

Query Match 100.0%; Score 1102; DB 6; Length 212;

Best Local Similarity 100.0%; Pred. No. 5.8e-114;
Matches 212; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLWLLPFLVTAIHAEICQPGAENAFKVRLLSIRLTALGDKAYAWDTNEEYLFKAMVAFSMRK 60
Db 1 MLWLLPFLVTAIHAEICQPGAENAFKVRLLSIRLTALGDKAYAWDTNEEYLFKAMVAFSMRK 60
QY 61 VPNREATEISHVLLCNVTQVRVSFWFVVTDPSPKHTLPAVEVQSAIRMKRINNAFFLND 120

Db 61 VPNREATEISHVLLCNVTQVSFWFVVTDPSKNHTLPAVEVQSAIRNMKNRINNAFFLND 120
Qy 121 QTLEFLKIPSTLAPPMDSVPPIWIIIFGVIFCIIIVAIALLILSGIWORRRKNKEPSEVD 180
Db 121 QTLEFLKIPSTLAPPMDSVPPIWIIIFGVIFCIIIVAIALLILSGIWORRRKNKEPSEVD 180
Qy 181 DAEDKCNMITIENGIPSDPLDMKGGIIMMPS 212
Db 181 DAEDKCNMITIENGIPSDPLDMKGGIIMMPS 212

RESULT 11

ABU13980

ID ABU13980 standard; protein; 212 AA.

XX

AC ABU13980;

XX

DT 26-FEB-2003 (first entry)

XX

DE Human PRO1312 polypeptide.

XX

KW Human; PRO polypeptide; secreted protein; transmembrane protein;
genetic disorder; antibacterial; immunosuppressive.

XX

OS Homo sapiens.

XX

PN US2002103125-A1.

XX

PD 01-AUG-2002.

XX

PF 20-NOV-2001; 2001US-00989731.

XX

PR 16-JUN-1997; 97US-0049787P.

PR 17-OCT-1997; 97US-0062250P.

PR 05-NOV-1997; 97WO-US020069.

PR 12-NOV-1997; 97US-0065186P.

PR 13-NOV-1997; 97US-0065311P.

PR 24-NOV-1997; 97US-0066770P.

PR 25-FEB-1998; 98US-0075945P.

PR 20-MAR-1998; 98US-0078910P.

PR 28-APR-1998; 98US-0083322P.

PR 07-MAY-1998; 98US-0084600P.

PR 28-MAY-1998; 98US-0087106P.

PR 02-JUN-1998; 98US-0087607P.

PR 02-JUN-1998; 98US-0087609P.

PR 02-JUN-1998; 98US-0087759P.

PR 03-JUN-1998; 98US-0087827P.

PR 04-JUN-1998; 98US-0088021P.

PR 04-JUN-1998; 98US-0088025P.

PR 04-JUN-1998; 98US-0088026P.

PR 04-JUN-1998; 98US-0088028P.

PR 04-JUN-1998; 98US-0088029P.

PR 04-JUN-1998; 98US-0088030P.

PR 04-JUN-1998; 98US-0088033P.

PR 04-JUN-1998; 98US-0088326P.

PR 05-JUN-1998; 98US-0088167P.

PR 05-JUN-1998; 98US-0088202P.

PR 05-JUN-1998; 98US-0088212P.

PR 05-JUN-1998; 98US-0088217P.

PR 09-JUN-1998; 98US-0088655P.

PR 10-JUN-1998; 98US-0088734P.

PR 10-JUN-1998; 98US-0088738P.

PR 10-JUN-1998; 98US-0088742P.

PR 10-JUN-1998; 98US-0088810P.

PR 10-JUN-1998; 98US-0088824P.

PR 10-JUN-1998; 98US-0088826P.

PR 11-JUN-1998; 98US-0088958P.

PR 11-JUN-1998; 98US-0088861P.

PR 11-JUN-1998; 98US-0088876P.

PR 12-JUN-1998; 98US-0089105P.

PR 16-JUN-1998; 98US-0089440P.

PR 16-JUN-1998; 98US-0089512P.

PR 16-JUN-1998; 98US-0089514P.

PR 17-JUN-1998; 98US-0089532P.
PR 17-JUN-1998; 98US-0089538P.
PR 17-JUN-1998; 98US-0089598P.
PR 17-JUN-1998; 98US-0089599P.
PR 17-JUN-1998; 98US-0089600P.
PR 17-JUN-1998; 98US-0089653P.
PR 18-JUN-1998; 98US-0089801P.
PR 18-JUN-1998; 98US-0089907P.
PR 18-JUN-1998; 98US-0089908P.
PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98WO-US019437.
PR 07-OCT-1998; 98WO-US021141.
PR 01-DEC-1998; 98WO-US025108.
PR 05-JAN-1999; 99WO-US000106.
PR 08-MAR-1999; 99WO-US005028.
PR 02-JUN-1999; 99WO-US012252.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 30-NOV-1999; 99WO-US028313.
PR 01-DEC-1999; 99WO-US028301.
PR 01-DEC-1999; 99WO-US028634.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 06-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US004914.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 10-MAR-2000; 2000WO-US006319.
PR 15-MAR-2000; 2000WO-US006884.
PR 20-MAR-2000; 2000WO-US007377.
PR 30-MAR-2000; 2000WO-US008439.
PR 15-MAY-2000; 2000WO-US013358.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 11-AUG-2000; 2000WO-US022031.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000WO-US030952.
PR 01-DEC-2000; 2000WO-US032678.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-JUN-2001; 2001WO-US017800.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 28-AUG-2001; 2001US-00941992.
XX
PA (GETH) GENENTECH LTD.
XX
PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
PI Ferrara N, Pong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi JC, Gurney AL, Kljavin IJ, Napier MA, Pan J, Paoni NP;
PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;
PI Zhang Z;
XX
DR WPI; 2003-102117/09.
DR N-PSDB; ABX64194.
XX
PT Novel secreted and transmembrane polypeptide for modulating biological
PT activity of cell expressing the polypeptide, identifying agonists or
PT antagonists of polypeptide, and as molecular weight markers.
XX
PS Claim 12; Fig 278; 649pp; English.
XX
CC The present invention relates to the isolation of novel human PRO
CC polypeptides, and the polynucleotide sequences encoding them. The PRO
CC polypeptides are secreted and transmembrane proteins. The PRO

polypeptides are useful for detecting other PRO polypeptides, for linking bioactive molecules to cells expressing PRO polypeptides, for modulating biological activities of cells expressing PRO polypeptides, and for identifying agonists or antagonists. The polynucleotide sequences encoding PRO polypeptides are useful as hybridisation probes, in chromosome and gene mapping, in the generation of antisense RNA and DNA, in the preparation of PRO polypeptides, for generating transgenic animals or knockout animals, to construct hybridisation probes for mapping the gene which encodes the PRO polypeptide, and for the genetic analysis of individuals with genetic disorders, in gene therapy, for chromosome identification, as chromosome markers, and for generating probes for PCR, Northern analysis, Southern analysis and Western analysis. ABU13860-CC ABU14006 represent the human PRO polypeptides of the invention. Note: The sequence data for this patent was obtained in electronic format directly from the USPTO web site at seqdata.uspto.gov/psipsDIDEntry.html

XX SQ Sequence 212 AA;

Query Match 100.0%; Score 1102; DB 6; Length 212;
Best Local Similarity 100.0%; Pred. No. 5.8e-114;
Matches 212; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLWLLFLVTAIHAELCPGAENAFKVRLSIRTALGDKAYAWDTNBEYLFKAMVAFSMRK 60
Db 1 MLWLLFLVTAIHAELCPGAENAFKVRLSIRTALGDKAYAWDTNBEYLFKAMVAFSMRK 60
QY 61 VPNREATEISHVLLCNVTQVSFWFVVTDPSPKNHTLPAVEVQSAIRMKNRINNAPFLND 120
Db 61 VPNREATEISHVLLCNVTQVSFWFVVTDPSPKNHTLPAVEVQSAIRMKNRINNAPFLND 120
QY 121 QTLEFLKIPSTLAPPDPSVPIWIIIFGVIFCIIIVATALLILSGIWQRRRKNKEPSEVD 180
Db 121 QTLEFLKIPSTLAPPDPSVPIWIIIFGVIFCIIIVATALLILSGIWQRRRKNKEPSEVD 180
QY 181 DAEDKCNMITIENGIPSDPLDMKGGILMMP 212
Db 181 DAEDKCNMITIENGIPSDPLDMKGGILMMP 212

RESULT 12

ABU81110
ID ABU81110 standard; protein; 212 AA.
XX AC ABU81110;
XX DT 23-JUN-2003 (first entry)
XX DE Human PRO polypeptide #241.
XX KW Human; PRO polypeptide; secreted and transmembrane protein;
KW anti-PRO antibody; diagnostic assay; gene expression; diabetes;
KW bone disorder; cartilage disorder; rheumatoid arthritis; obesity;
KW sports injury; osteoarthritis; hyper-insulinaemia; hypo-insulinaemia;
KW hearing loss; coagulation disorder; stroke; heart attack; cardiac;
KW antidiabetic; anorectic; vulnery; antiarthritic; osteopathic;
KW antirheumatic; auditory; cerebroprotective; angiogenic.
XX OS Homo sapiens.
XX PN US2003004311-A1.
XX PD 02-JAN-2003.
XX PF 19-DEC-2001; 2001US-00028072.
XX PR 18-JUN-1997; 97US-0049911P.
PR 26-AUG-1997; 97US-0056974P.
PR 17-SEP-1997; 97US-0059113P.
PR 17-SEP-1997; 97US-0059115P.
PR 17-SEP-1997; 97US-0059117P.
PR 17-SEP-1997; 97US-0059122P.
PR 17-SEP-1997; 97US-0059184P.
PR 18-SEP-1997; 97US-0059263P.
PR 19-SEP-1997; 97US-0059352P.
PR 19-SEP-1997; 97US-0059588P.
PR 24-SEP-1997; 97US-0059836P.
PR 17-OCT-1997; 97US-0062250P.
PR 17-OCT-1997; 97US-0062285P.
PR 17-OCT-1997; 97US-0062287P.
PR 17-OCT-1997; 97US-0063755P.
PR 24-OCT-1997; 97US-0062814P.
PR 24-OCT-1997; 97US-0062816P.
PR 24-OCT-1997; 97US-0063045P.
PR 24-OCT-1997; 97US-0063082P.
PR 24-OCT-1997; 97US-0063127P.
PR 27-OCT-1997; 97US-0063327P.
PR 28-OCT-1997; 97US-0063329P.
PR 28-OCT-1997; 97US-0063550P.
PR 28-OCT-1997; 97US-0063561P.
PR 29-OCT-1997; 97US-0063704P.
PR 29-OCT-1997; 97US-0063733P.
PR 29-OCT-1997; 97US-0063735P.
PR 29-OCT-1997; 97US-0063738P.
PR 03-NOV-1997; 97US-0064248P.
PR 07-NOV-1997; 97US-0064809P.
PR 12-NOV-1997; 97US-0065186P.
PR 17-NOV-1997; 97US-0065846P.
PR 21-NOV-1997; 97US-0066364P.
PR 24-NOV-1997; 97US-0066453P.
PR 24-NOV-1997; 97US-0066511P.
PR 24-NOV-1997; 97US-0066770P.
PR 11-DEC-1997; 97US-0069212P.
PR 11-DEC-1997; 97US-0069278P.
PR 11-DEC-1997; 97US-0069334P.
PR 16-DEC-1997; 97US-0069694P.
PR 23-JAN-1998; 98US-0072320P.
PR 04-FEB-1998; 98US-0073612P.
PR 09-FEB-1998; 98US-0074086P.
PR 09-FEB-1998; 98US-0074092P.
PR 12-MAR-1998; 98US-0077791P.
PR 20-MAR-1998; 98US-0078910P.
PR 25-MAR-1998; 98US-0079294P.
PR 27-MAR-1998; 98US-0079663P.
PR 27-MAR-1998; 98US-0079728P.
PR 31-MAR-1998; 98US-0080165P.
PR 12-JUN-1998; 98WO-US012456.
PR 14-JUL-1998; 98WO-US014552.
PR 28-AUG-1998; 98WO-US017888.
PR 10-SEP-1998; 98WO-US018824.
PR 14-SEP-1998; 98WO-US019093.
PR 14-SEP-1998; 98WO-US019094.
PR 14-SEP-1998; 98WO-US019177.
PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98WO-US019437.
PR 07-OCT-1998; 98WO-US021141.
PR 29-OCT-1998; 98WO-US022391.
PR 29-OCT-1998; 98WO-US022392.
PR 20-NOV-1998; 98WO-US024855.
PR 01-DEC-1998; 98WO-US025108.
PR 05-JAN-1999; 99WO-US000106.
PR 08-MAR-1999; 99WO-US005028.
PR 10-MAR-1999; 99WO-US005196.
PR 20-APR-1999; 99WO-US008615.
PR 14-MAY-1999; 99WO-US010733.
PR 02-JUN-1999; 99WO-US012253.
PR 01-SEP-1999; 99WO-US020111.
PR 08-SEP-1999; 99WO-US020594.
PR 13-SEP-1999; 99WO-US020944.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 05-OCT-1999; 99WO-US023089.
PR 29-NOV-1999; 99WO-US028214.
PR 30-NOV-1999; 99WO-US028313.
PR 30-NOV-1999; 99WO-US028409.
PR 01-DEC-1999; 99WO-US028301.
PR 01-DEC-1999; 99WO-US028634.

PR 18-JUN-1998; 98US-0089907P.
 PR 18-JUN-1998; 98US-0089908P.
 PR 16-SEP-1998; 98WO-US019330.
 PR 17-SEP-1998; 98WO-US019437.
 PR 07-OCT-1998; 98WO-US021141.
 PR 01-DEC-1998; 98WO-US025108.
 PR 05-JAN-1999; 98WO-US000106.
 PR 08-MAR-1999; 99WO-US005028.
 PR 02-JUN-1999; 99WO-US012252.
 PR 15-SEP-1999; 99WO-US021090.
 PR 15-SEP-1999; 99WO-US021547.
 PR 30-NOV-1999; 99WO-US028313.
 PR 01-DEC-1999; 99WO-US028301.
 PR 01-DEC-1999; 99WO-US028634.
 PR 16-DEC-1999; 99WO-US030095.
 PR 20-DEC-1999; 99WO-US030911.
 PR 05-JAN-2000; 2000WO-US000219.
 PR 06-JAN-2000; 2000WO-US000376.
 PR 11-FEB-2000; 2000WO-US003565.
 PR 18-FEB-2000; 2000WO-US004341.
 PR 22-FEB-2000; 2000WO-US004414.
 PR 24-FEB-2000; 2000WO-US004914.
 PR 24-FEB-2000; 2000WO-US005004.
 PR 02-MAR-2000; 2000WO-US005841.
 PR 10-MAR-2000; 2000WO-US006319.
 PR 15-MAR-2000; 2000WO-US006884.
 PR 20-MAR-2000; 2000WO-US007377.
 PR 30-MAR-2000; 2000WO-US008439.
 PR 15-MAY-2000; 2000WO-US013358.
 PR 17-MAY-2000; 2000WO-US013705.
 PR 22-MAY-2000; 2000WO-US014042.
 PR 30-MAY-2000; 2000WO-US014941.
 PR 02-JUN-2000; 2000WO-US015264.
 PR 28-JUL-2000; 2000WO-US020710.
 PR 11-AUG-2000; 2000WO-US022031.
 PR 23-AUG-2000; 2000WO-US023522.
 PR 24-AUG-2000; 2000WO-US023328.
 PR 08-NOV-2000; 2000WO-US030952.
 PR 01-DEC-2000; 2000WO-US032678.
 PR 28-FEB-2001; 2001WO-US006520.
 PR 01-JUN-2001; 2001WO-US017800.
 PR 20-JUN-2001; 2001WO-US019692.
 PR 29-JUN-2001; 2001WO-US021066.
 PR 09-JUL-2001; 2001WO-US021735.
 PR 28-AUG-2001; 2001US-00941992.
 (GETH) GENENTECH INC.
 PA Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
 PI Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ;
 PI Grimaldi JC, Gurney AL, Kljavin IJ, Napier MA, Pan J, Paoni NF;
 PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;
 PI Zhang Z;
 XX WPI; 2003-352829/33.
 DR N-PSDB; ACA64416.
 XX
 PT New genes and secreted and transmembrane polypeptides (e.g. PRO183 or
 PT PRO184), useful for treating or diagnosing e.g. ovarian cancer, Kaposi's
 PT sarcoma, leukemia, lymphoma, hepatitis B, multiple sclerosis or Crohn's
 PT disease.
 XX
 PS Claim 12; Fig 278; 663pp; English.
 XX
 CC The invention describes a new isolated nucleic acid molecule comprising
 CC the full length coding sequence of the DNA deposited with the American
 CC Type Culture Collection (e.g. ATCC Deposit No. 209621, 552-PTA, 819-PTA,
 CC 209439, 203135, etc); or a sequence with at least 80% identity to a DNA
 CC encoding a PRO polypeptide. The PRO polypeptides or polynucleotides are
 CC useful as pharmaceuticals, diagnostics, biosensors or bioreactors. These
 CC are particularly useful for detecting or treating e.g. malignancies or
 CC cancers (e.g. ovarian cancer, colorectal cancer, Kaposi's sarcoma,
 CC leukaemia or lymphoma), hepatitis B, multiple sclerosis, or Crohn's

CC disease in mammals. The PRO polypeptides are useful in drug screening,
 CC particularly as targets for therapeutic intervention in these diseases,
 CC and in the diagnostic determination of the presence of these diseases.
 CC The PRO polypeptides are also useful as molecular weight markers, or for
 CC chromosome identification. The PRO genes are useful as hybridisation
 CC probes, or for screening libraries of human cDNA, genomic DNA or mRNA.
 CC The PRO genes may also be used in gene therapy, particularly for
 CC replacing a defective gene. This is the amino acid sequence of a novel
 CC human secreted and transmembrane PRO polypeptide
 XX
 SQ Sequence 212 AA;
 Query Match 100.0%; Score 1102; DB 6; Length 212;
 Best Local Similarity 100.0%; Pred. No. 5.8e-114;
 Matches 212; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MLWLLFFLVTAIHAELCQPGAENAFKVRLSIRLTALGDKAYAWDTNEYLYFKAMVAFSMRK 60
 Db 1 MLWLLFFLVTAIHAELCQPGAENAFKVRLSIRLTALGDKAYAWDTNEYLYFKAMVAFSMRK 60
 QY 61 VPNREATEISHVLLCNVTQVSFVFVTDPSKNHTLPAAVEVQSAIRNMKNRINNAFFLND 120
 Db 61 VPNREATEISHVLLCNVTQVSFVFVTDPSKNHTLPAAVEVQSAIRNMKNRINNAFFLND 120
 QY 121 QTLFLKIPSTLAPPMDPSVPIWIIIFGVIFCIIVAIALLLSGIWQRRRNKKEPSEVD 180
 Db 121 QTLFLKIPSTLAPPMDPSVPIWIIIFGVIFCIIVAIALLLSGIWQRRRNKKEPSEVD 180
 QY 181 DAEDKCNMTIENGIPSDPLDMKGILMMP 212
 Db 181 DAEDKCNMTIENGIPSDPLDMKGILMMP 212
 RESULT 14
 ABU66810
 ID ABU66810 standard; protein; 212 AA.
 XX
 AC ABU66810;
 XX
 DT 23-MAY-2003 (first entry)
 XX
 DE Human PRO polypeptide #241.
 XX
 KW Human; PRO polypeptide; secreted and transmembrane protein;
 KW tumour necrosis factor-alpha; TNF-alpha; blood; proliferation;
 KW differentiation; chondrocyte; tumour; genetic disorder; cytostatic.
 XX
 OS Homo sapiens.
 XX
 PN US2003036180-A1.
 XX
 PD 20-FEB-2003.
 XX
 PF 09-MAY-2002; 2002US-00143114.
 XX
 PR 31-MAR-1997; 97WO-US005230.
 PR 12-JUN-1998; 98WO-US012456.
 PR 14-JUL-1998; 98WO-US014552.
 PR 28-AUG-1998; 98WO-US017888.
 PR 10-SEP-1998; 98WO-US018824.
 PR 14-SEP-1998; 98WO-US019093.
 PR 14-SEP-1998; 98WO-US019094.
 PR 14-SEP-1998; 98WO-US019177.
 PR 16-SEP-1998; 98WO-US019330.
 PR 17-SEP-1998; 98WO-US019437.
 PR 07-OCT-1998; 98WO-US021141.
 PR 29-OCT-1998; 98WO-US022991.
 PR 29-OCT-1998; 98WO-US022992.
 PR 20-NOV-1998; 98WO-US024855.
 PR 01-DEC-1998; 98WO-US025108.
 PR 05-JAN-1999; 99WO-US000106.
 PR 08-MAR-1999; 99WO-US005028.
 PR 10-MAR-1999; 99WO-US005190.

PR 20-APR-1999; 99WO-US008615.
PR 14-MAY-1999; 99WO-US010733.
PR 02-JUN-1999; 99WO-US012252.
PR 01-SEP-1999; 99WO-US020111.
PR 08-SEP-1999; 99WO-US020594.
PR 13-SEP-1999; 99WO-US020944.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 05-OCT-1999; 99WO-US023089.
PR 29-NOV-1999; 99WO-US028214.
PR 30-NOV-1999; 99WO-US028313.
PR 30-NOV-1999; 99WO-US028409.
PR 01-DEC-1999; 99WO-US028301.
PR 01-DEC-1999; 99WO-US028634.
PR 02-DEC-1999; 99WO-US028551.
PR 02-DEC-1999; 99WO-US028564.
PR 02-DEC-1999; 99WO-US028565.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 20-DEC-1999; 99WO-US030999.
PR 22-DEC-1999; 99WO-US030720.
PR 30-DEC-1999; 99WO-US031243.
PR 30-DEC-1999; 99WO-US031274.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000277.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 18-FEB-2000; 2000WO-US004342.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US004914.
PR 24-FEB-2000; 2000WO-US005004.
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005746.
PR 02-MAR-2000; 2000WO-US005841.
PR 10-MAR-2000; 2000WO-US006319.
PR 15-MAR-2000; 2000WO-US006884.
PR 20-MAR-2000; 2000WO-US007377.
PR 21-MAR-2000; 2000WO-US007532.
PR 30-MAR-2000; 2000WO-US008439.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 11-AUG-2000; 2000WO-US022031.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000WO-US030952.
PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001US-00796498.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-MAR-2001; 2001WO-US006666.
PR 09-MAR-2001; 2001US-00802706.
PR 14-MAR-2001; 2001US-00808689.
PR 22-MAR-2001; 2001US-00816744.
PR 05-APR-2001; 2001US-00828366.
PR 10-MAY-2001; 2001US-00854208.
PR 10-MAY-2001; 2001US-00854280.
PR 18-MAY-2001; 2001US-00860216.
PR 25-MAY-2001; 2001US-00866028.
PR 25-MAY-2001; 2001US-00866034.
PR 25-MAY-2001; 2001WO-US017092.
PR 01-JUN-2001; 2001US-00872035.
PR 01-JUN-2001; 2001WO-US017800.
PR 05-JUN-2001; 2001US-00874503.
PR 14-JUN-2001; 2001US-00882636.
PR 19-JUN-2001; 2001US-00886342.
PR 20-JUN-2001; 2001WO-US019692.
PR 21-JUN-2001; 2001US-00887879.

PR 22-JUN-2001; 2001WO-US020116.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 18-JUL-2001; 2001US-00908827.
PR 06-AUG-2001; 2001US-00924419.
PR 09-AUG-2001; 2001US-00927796.
PR 16-AUG-2001; 2001US-00931836.
PR 19-DEC-2001; 2001US-00028072.
XX
PA (GETH) GENENTECH INC.
XX
XX
PI Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;
PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
XX
DR WPI; 2003-332040/31.
DR N-PSDB; ACA03843.
XX
PT New secreted and transmembrane PRO nucleic acids, useful for gene
PT therapy, in chromosome and gene mapping, as chromosome markers, in tissue
PT typing, and in chromosome identification.
XX
PS Claim 12; Fig 482; 660pp; English.
XX
CC The present invention relates to the isolation of novel human PRO
CC polypeptides, and the polynucleotide sequences encoding them. The PRO
CC polypeptides are secreted and transmembrane proteins. The PRO
CC polypeptides are useful for detecting other PRO polypeptides, for linking
CC bioactive molecules to cells expressing PRO polypeptides, for modulating
CC biological activities of cells expressing PRO polypeptides, and for
CC identifying agonists or antagonists. The PRO polypeptides are useful for
CC for stimulating the release of tumour necrosis factor (TNF)-alpha from
CC human blood, for stimulating the proliferation or differentiation of
CC chondrocytes, and detecting the presence of tumours. The polynucleotide
CC sequences encoding PRO polypeptides are useful as hybridisation probes,
CC in chromosome and gene mapping, in the generation of antisense RNA and
CC DNA, in the preparation of PRO polypeptides, for generating transgenic
CC animals or knockout animals, for the genetic analysis of individuals with
CC genetic disorders, and in gene therapy. ABU6570-ABU65844 represent the
CC human PRO polypeptides of the invention. Note: The sequence data for this
CC patent was obtained in electronic format directly from the USPTO web site
CC at seqdata.uspto.gov/psipsDIDentry.html
XX
SQ Sequence 212 AA;
Query Match 100.0%; Score 1102; DB 6; Length 212;
Best Local Similarity 100.0%; Pred. No. 5.8e-114;
Matches 212; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 MLWLLFFLVTAIHAELCQPGAENAFKVLRSIRFALGDKAYAWDTNEEYLFKAMVAFSMRK 60
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Db 61 VPNREATEISHVLLCNVTQVSFWFVVTDPSPKNTLPAAVEVQSAIRMKNRINNAPFLND 120
Qy 121 QTLEFLKIPSTLAPPMDSVPIWIIIFGVIFCIIIVAIALLISGIWQRRRKNKBPSEVD 180
Db 121 QTLEFLKIPSTLAPPMDSVPIWIIIFGVIFCIIIVAIALLISGIWQRRRKNKBPSEVD 180
Qy 181 DAEDKCNMTIENGIPSDPLDMKGGLAMPS 212
Db 181 DAEDKCNMTIENGIPSDPLDMKGGLAMPS 212
RESULT 15
ABU59891
ID ABU59891 standard; protein; 212 AA.
XX
AC ABU59891;
XX
DT 13-MAY-2003 (first entry)

XX Novel secreted and transmembrane protein PRO1312.
DE Human; PRO; hypertrophy of neonatal heart; angiogenesis; wound healing;
XX cardiac insufficiency disorder; cancer; tumour; immune response;
KW adrenal cortical capillary endothelial growth; c-fos induction;
KW vascular endothelial growth factor inhibition; VEGF inhibition;
KW endothelial cell growth inhibitor; T-lymphocytes stimulation;
KW retinal neurons cell survival; rod photoreceptor cell survival;
KW mammalian kidney mesangial cell proliferation; kidney disease;
KW dermatitis; herpeticiformis; Crohn's disease; chondrocyte proliferation;
KW chondrocyte redifferentiation; sports injury; arthritis.
XX Homo sapiens.
XX US2003017563-A1.
XX 23-JAN-2003.
XX 07-MAY-2002; 2002US-00140808.
PR 31-MAR-1997; 97WO-US005230.
PR 12-JUN-1998; 98WO-US012456.
PR 14-JUL-1998; 98WO-US014552.
PR 28-AUG-1998; 98WO-US017888.
PR 10-SEP-1998; 98WO-US018824.
PR 14-SEP-1998; 98WO-US019093.
PR 14-SEP-1998; 98WO-US019094.
PR 14-SEP-1998; 98WO-US019177.
PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98WO-US019437.
PR 07-OCT-1998; 98WO-US021141.
PR 29-OCT-1998; 98WO-US022991.
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PR 20-NOV-1998; 98WO-US024855.
PR 01-DEC-1998; 98WO-US025108.
PR 05-JAN-1999; 99WO-US000106.
PR 08-MAR-1999; 99WO-US005028.
PR 10-MAR-1999; 99WO-US005190.
PR 20-APR-1999; 99WO-US008615.
PR 14-MAY-1999; 99WO-US010733.
PR 02-JUN-1999; 99WO-US012252.
PR 01-SEP-1999; 99WO-US020111.
PR 08-SEP-1999; 99WO-US020594.
PR 13-SEP-1999; 99WO-US020944.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 05-OCT-1999; 99WO-US023089.
PR 29-NOV-1999; 99WO-US028214.
PR 30-NOV-1999; 99WO-US028313.
PR 30-NOV-1999; 99WO-US028409.
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PR 02-DEC-1999; 99WO-US028564.
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PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 20-DEC-1999; 99WO-US030999.
PR 22-DEC-1999; 99WO-US030720.
PR 30-DEC-1999; 99WO-US031243.
PR 30-DEC-1999; 99WO-US031274.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000277.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 18-FEB-2000; 2000WO-US004342.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US004914.
PR 24-FEB-2000; 2000WO-US005004.
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005746.
PR 02-MAR-2000; 2000WO-US005841.
PR 10-MAR-2000; 2000WO-US006319.
PR 15-MAR-2000; 2000WO-US006884.
PR 20-MAR-2000; 2000WO-US007377.
PR 21-MAR-2000; 2000WO-US007532.
PR 30-MAR-2000; 2000WO-US008439.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 11-AUG-2000; 2000WO-US022031.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000WO-US030952.
PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001US-00796498.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-MAR-2001; 2001WO-US006666.
PR 09-MAR-2001; 2001US-00802706.
PR 14-MAR-2001; 2001US-00808689.
PR 22-MAR-2001; 2001US-00816744.
PR 05-APR-2001; 2001US-00828366.
PR 10-MAY-2001; 2001US-00854208.
PR 10-MAY-2001; 2001US-00854280.
PR 25-MAY-2001; 2001US-00866028.
PR 25-MAY-2001; 2001US-00866034.
PR 25-MAY-2001; 2001WO-US017092.
PR 01-JUN-2001; 2001US-00872035.
PR 01-JUN-2001; 2001WO-US017800.
PR 05-JUN-2001; 2001US-00874503.
PR 14-JUN-2001; 2001US-00882636.
PR 19-JUN-2001; 2001US-00886342.
PR 20-JUN-2001; 2001WO-US019692.
PR 21-JUN-2001; 2001US-00887879.
PR 22-JUN-2001; 2001WO-US020116.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 18-JUL-2001; 2001US-00908827.
PR 06-AUG-2001; 2001US-00924419.
PR 09-AUG-2001; 2001US-00927796.
PR 16-AUG-2001; 2001US-00931836.
PR 19-DEC-2001; 2001US-00028072.
XX (GETH) GENENTECH INC.
PA Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;
PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
XX WPI; 2003-148238/14.
DR N-PSDB; ABX89381.
XX Two hundred and seventy five nucleic acids encoding PRO polypeptides,
PT useful for treating pericyte-associated tumors, diabetes and various bone
PT and/or cartilage disorders, e.g. arthritis.
XX Claim 12; Fig 482; 659pp; English.
XX The invention describes an isolated human PRO polypeptide. The PRO
CC polypeptides are useful in detecting PRO polypeptides in a sample, in
CC linking a bioactive molecule to a cell expressing a PRO polypeptide, and
CC in modulating at least one biological activity of a cell expressing a PRO
CC polypeptide. PRO1312 stimulates hypertrophy of neonatal heart and is thus
CC useful for treating cardiac insufficiency disorders. PRO1154 and PRO1186
CC stimulate adrenal cortical capillary endothelial growth, and PRO536,
CC PRO943, PRO828, PRO826, PRO1068 or PRO535, PRO826, PRO819, PRO1126,
CC PRO1360 and PRO1387 induce c-fos in endothelial cells, and are thus

CC useful for treating conditions or disorders where angiogenesis would be
CC beneficial, e.g. wound healing and antagonist of this polypeptide are
CC useful for treating cancerous tumours. PRO812 inhibits vascular
CC endothelial growth factor (VEGF) stimulated proliferation of endothelial
CC cells and is thus useful for inhibiting endothelial cell growth in
CC mammals which would be beneficial in inhibiting tumour growth. PRO826,
CC PRO1068, PRO1184, PRO1346 and PRO1375 stimulate proliferation of
CC stimulated T-lymphocytes and are therapeutically useful for enhancing
CC immune response. PRO828, PRO826, PRO1068 or PRO1132 enhance survival of
CC retinal neurons cells (PRO1132 is also enhances survival/proliferation of
CC rod photoreceptor cells) and therefore are useful for treating retinal
CC disorders of injuries, e.g. retinitis pigmentosum, AMD. PRO819, PRO813
CC and PRO1066 induce proliferation of mammalian kidney mesangial cells,
CC and therefore are useful for treating kidney disorders associated with
CC decreased mesangial cell function such as Berger disease or Crohn's
CC nephropathies associated with dermatitis, herpetiformis or other
CC disease. PRO1310, PRO844, PRO1312, PRO1192 and PRO1387 induce the
CC proliferation and/or redifferentiation of chondrocytes in culture and are
CC thus useful for treating sports injuries, and arthritis. This is the
CC amino acid sequence of a novel human PRO protein
XX
SQ Sequence 212 AA;

Query Match 100.0%; Score 1102; DB 6; Length 212;
Best Local Similarity 100.0%; Pred. No. 5.8e-114;
Matches 212; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLWLLFFLVTAIHAELCQPGAENAPKVRLSIRTALGDKAYAWDTNEBYLFKAMVAFSMRK 60
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QY 61 VPNREATEISHVLLCNVTQVSFWFVVTDPKSNHTLPAVEVQSARIMNKRINNAPFLND 120
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121 QTLEFLKIPSTLAPPMDPSVPIWIIIFGVIFCIIIVAIALLILSGIWQRRRKNKPSEVD 180

QY 181 DAEDKCNMTIENGIPSDPLDMKGGIIMMPS 212
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
181 DAEDKCNMTIENGIPSDPLDMKGGIIMMPS 212

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 31, 2004, 12:04:05 ; Search time 23 Seconds
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475.857 Million cell updates/sec

Title: US-09-989-724-387
Perfect score: 1102
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
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5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	376	34.1	805	3	US-08-989-299-2 Sequence 2, Appli
2	376	34.1	805	4	US-10-158-847-142 Sequence 142, Appl
3	376	34.1	805	4	US-09-407-427-2 Sequence 2, Appli
4	359	32.6	711	4	US-10-158-847-138 Sequence 138, Appl
5	289	26.2	681	4	US-10-158-847-140 Sequence 140, Appl
6	90	8.2	799	1	US-08-188-228-42 Sequence 42, Appl
7	90	8.2	799	1	US-08-332-638-42 Sequence 42, Appl
8	89.5	8.1	793	1	US-08-188-228-54 Sequence 54, Appl
9	89.5	8.1	793	1	US-08-332-643-48 Sequence 48, Appl
10	89.5	8.1	793	1	US-08-332-638-54 Sequence 54, Appl
11	88	8.0	363	1	US-07-946-497-7 Sequence 7, Appli
12	88	8.0	363	1	US-08-483-322-7 Sequence 7, Appli
13	88	8.0	363	2	US-08-478-882-7 Sequence 7, Appli
14	86	7.8	503	1	US-07-946-497-2 Sequence 2, Appli
15	86	7.8	503	1	US-08-483-322-2 Sequence 2, Appli
16	86	7.8	503	2	US-08-478-882-2 Sequence 2, Appli
17	84.5	7.7	339	2	US-08-892-880-3 Sequence 3, Appli
18	83.5	7.6	1337	3	US-08-854-585-2 Sequence 2, Appli
19	83.5	7.6	1337	4	US-09-447-533-2 Sequence 2, Appli
20	83.5	7.6	1337	5	PCT-US95-05512-2 Sequence 2, Appli
21	82.5	7.5	529	4	US-09-134-000C-5948 Sequence 5948, Ap
22	78.5	7.1	438	4	US-09-404-879A-390 Sequence 390, App
23	78.5	7.1	833	4	US-09-404-879A-389 Sequence 389, App
24	78.5	7.1	914	4	US-09-404-879A-312 Sequence 312, App
25	78.5	7.1	914	4	US-09-338-933-312 Sequence 312, App
26	75.5	6.9	944	4	US-09-107-532A-4864 Sequence 4864, Ap
27	75.5	6.9	2035	2	US-08-479-537A-2 Sequence 2, Appli

28	75.5	6.9	2035	3	US-09-083-116-2	Sequence 2, Appli
29	75.5	6.9	2035	4	US-09-134-916A-2	Sequence 2, Appli
30	75	6.8	1260	3	US-09-245-041-2	Sequence 2, Appli
31	73.5	6.7	298	1	US-08-118-270-76	Sequence 76, Appl
32	73.5	6.7	298	5	PCT-US93-08528-76	Sequence 76, Appl
33	73.5	6.7	562	4	US-09-489-039A-8574	Sequence 8574, Ap
34	73.5	6.7	796	2	US-08-738-349-2	Sequence 2, Appli
35	73	6.6	14	3	US-08-905-223-28	Sequence 28, Appl
36	73	6.6	14	4	US-09-247-155-28	Sequence 28, Appl
37	73	6.6	14	4	US-09-663-600A-28	Sequence 28, Appl
38	73	6.6	14	4	US-09-621-976-6	Sequence 6, Appli
39	73	6.6	195	4	US-09-543-681A-7985	Sequence 7985, Ap
40	72.5	6.6	299	4	US-09-651-200-15	Sequence 15, Appl
41	72	6.5	283	2	US-08-332-562A-136	Sequence 136, App
42	72	6.5	510	4	US-09-540-236-2148	Sequence 2148, Ap
43	71.5	6.5	796	1	US-08-188-228-58	Sequence 58, Appl
44	71.5	6.5	796	1	US-08-332-643-52	Sequence 52, Appl
45	71.5	6.5	796	1	US-08-332-638-58	Sequence 58, Appl

ALIGNMENTS

RESULT 1
US-08-989-299-2
; Sequence 2, Application US/08989299
; Patent No. 6194556
; GENERAL INFORMATION:
; APPLICANT: Acton, Susan L.
; APPLICANT: Robinson, Keith E.
; TITLE OF INVENTION: ANGIOTENSIN CONVERTING ENZYME HOMOLOG
; TITLE OF INVENTION: AND THERAPEUTIC AND DIAGNOSTIC USES THEREFOR
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY, HOAG & ELIOT LLP
; STREET: One Post Office Square
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109-2170
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/989,299
; FILING DATE: 11-DEC-1997
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Arnold E., Beth
; REGISTRATION NUMBER: 35,430
; REFERENCE/DOCKET NUMBER: MIA-025.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-832-1000
; TELEFAX: 617-832-7000
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 805 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-989-299-2

Query Match 34.1%; Score 376; DB 3; Length 805;
Best Local Similarity 47.9%; Pred. No. 1.4e-34;
Matches 79; Conservative 32; Mismatches 48; Indels 6; Gaps 3;
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Db 672 VANLKPRISFNFFVTAPKNVSDIIPRTEVEKAIKMSRSRINDAFRLNDSLEFLGIQPTL 731
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Db 732 GPPNQPPVSIWLIVFGVMGVIVGVIVILFTGIRDKKNKARS 776
RESULT 2
US-10-158-847-142
; Sequence 142, Application US/10158847
; Patent No. 6592865
; GENERAL INFORMATION:
; APPLICANT: Tom Parry et al.
; TITLE OF INVENTION: Method and Compositions for Modulating ACE-2 Activity
; FILE REFERENCE: PF557
; CURRENT APPLICATION NUMBER: US/10/158,847
; CURRENT FILING DATE: 2002-06-03
; PRIOR APPLICATION NUMBER: 60/295,004
; PRIOR FILING DATE: 2001-06-04
; NUMBER OF SEQ ID NOS: 158
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 142
; LENGTH: 805
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-158-847-142

Query Match 34.1%; Score 376; DB 4; Length 805;
Best Local Similarity 47.9%; Pred. No. 1.4e-34;
Matches 79; Conservative 32; Mismatches 48; Indels 6; Gaps 3;
QY 19 PGAENAFKVRLSIRITAGDKAYAWDTNNEEYLFKAMVAFSMR----KVPNREAT-EISHVL 73
Db 612 PYADQSIKVRISLKSALGDKAYENDNEMYLFRSSVAYAMRQYFLKVKQNMILFGEDVR 671
QY 74 LCVNTRQVSFWFVVTDPK-NHTLPAVEVQSAIRNMKNRINNAPFLNDQTLFLKIPSTL 132
Db 672 VANLKPRISFNFFVTAPKNVSDIIPRTEVEKAIKMSRSRINDAFRLNDSLEFLGIQPTL 731
QY 133 APPMDPSVPIWIIIFGVFCIIIVAIALLILSGIWQRRRKNKEPS 177
Db 732 GPPNQPPVSIWLIVFGVMGVIVGVIVILFTGIRDKKNKARS 776

RESULT 3
US-09-407-427-2
; Sequence 2, Application US/09407427
; Patent No. 6610497
; GENERAL INFORMATION:
; APPLICANT: Acton, Susan L.
; APPLICANT: Robison, Keith E.
; TITLE OF INVENTION: ANGIOTENSIN CONVERTING ENZYME HOMOLOG AND THERAPEUTIC
; TITLE OF INVENTION: AND DIAGNOSTIC USES THEREFOR
; FILE REFERENCE: MNI-132CP2
; CURRENT APPLICATION NUMBER: US/09/407,427
; CURRENT FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 09/163,648
; PRIOR FILING DATE: 1998-09-30
; PRIOR APPLICATION NUMBER: 08/989,299
; PRIOR FILING DATE: 1997-12-11
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 805
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-407-427-2

Query Match 34.1%; Score 376; DB 4; Length 805;
Best Local Similarity 47.9%; Pred. No. 1.4e-34;
Matches 79; Conservative 32; Mismatches 48; Indels 6; Gaps 3;

QY 19 PGAENAFKVRLSIRITAGDKAYAWDTNNEEYLFKAMVAFSMR----KVPNREAT-EISHVL 73
Db 612 PYADQSIKVRISLKSALGDKAYENDNEMYLFRSSVAYAMRQYFLKVKQNMILFGEDVR 671
QY 74 LCVNTRQVSFWFVVTDPK-NHTLPAVEVQSAIRNMKNRINNAPFLNDQTLFLKIPSTL 132
Db 672 VANLKPRISFNFFVTAPKNVSDIIPRTEVEKAIKMSRSRINDAFRLNDSLEFLGIQPTL 731
QY 133 APPMDPSVPIWIIIFGVFCIIIVAIALLILSGIWQRRRKNKEPS 177
Db 732 GPPNQPPVSIWLIVFGVMGVIVGVIVILFTGIRDKKNKARS 776
RESULT 4
US-10-158-847-138
; Sequence 138, Application US/10158847
; Patent No. 6592865
; GENERAL INFORMATION:
; APPLICANT: Tom Parry et al.
; TITLE OF INVENTION: Method and Compositions for Modulating ACE-2 Activity
; FILE REFERENCE: PF557
; CURRENT APPLICATION NUMBER: US/10/158,847
; CURRENT FILING DATE: 2002-06-03
; PRIOR APPLICATION NUMBER: 60/295,004
; PRIOR FILING DATE: 2001-06-04
; NUMBER OF SEQ ID NOS: 158
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 138
; LENGTH: 711
; TYPE: PRT
; ORGANISM: homo sapiens
; NAME/KEY: MISC FEATURE
; LOCATION: (219)..(219)
; OTHER INFORMATION: Xaa equals any amino acid
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (240)..(240)
; OTHER INFORMATION: Xaa equals any amino acid
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (499)..(499)
; OTHER INFORMATION: Xaa equals any amino acid
US-10-158-847-138

Query Match 32.6%; Score 359; DB 4; Length 711;
Best Local Similarity 47.2%; Pred. No. 1.1e-32;
Matches 75; Conservative 32; Mismatches 46; Indels 6; Gaps 3;
QY 19 PGAENAFKVRLSIRITAGDKAYAWDTNNEEYLFKAMVAFSMR----KVPNREAT-EISHVL 73
Db 551 PYADQSIKVRISLKSALGDKAYENDNEMYLFRSSVAYAMRQYFLKVKQNMILFGEDVR 610
QY 74 LCVNTRQVSFWFVVTDPK-NHTLPAVEVQSAIRNMKNRINNAPFLNDQTLFLKIPSTL 132
Db 611 VANLKPRISFNFFVTAPKNVSDIIPRTEVEKAIKMSRSRINDAFRLNDSLEFLGIQPTL 670
QY 133 APPMDPSVPIWIIIFGVFCIIIVAIALLILSGIWQRRR 171
Db 671 GPPNQPPVSIWLIVFGVMGVIVGVIVILFTGIRDK 709

RESULT 5
US-10-158-847-140
; Sequence 140, Application US/10158847
; Patent No. 6592865
; GENERAL INFORMATION:
; APPLICANT: Tom Parry et al.
; TITLE OF INVENTION: Method and Compositions for Modulating ACE-2 Activity
; FILE REFERENCE: PF557
; CURRENT APPLICATION NUMBER: US/10/158,847
; CURRENT FILING DATE: 2002-06-03
; PRIOR APPLICATION NUMBER: 60/295,004


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; TELEFAX: (312) 474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 42:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 799 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-332-638-42

Query Match      8.2%; Score 90; DB 1; Length 799;
Best Local Similarity 21.4%; Pred. No. 0.2;
Matches 52; Conservative 34; Mismatches 91; Indels 66; Gaps 11;

QY 13 HAEICQPGAENAFKVRLSIRLTALGDKAYAWDT-----NEEYLFKAMVAFSMRKVPN 63
Db 432 HTDLERQFNINADGKITLATPLDRELSVWHNIIATEIRNHSQISRVPVAIKVLDV-N 490
QY 64 REATEIS---HVLIC-----NVTQVSVFWVVTDPKSNH-----TLPAVEVQSAIRMNK 109
Db 491 DNAPEFASEYEAFLECGKPGQVIQTVSA-MDKDDPKNGHFFLYSLPEMNNPNFTIKK 549
QY 110 NRINNAPFL-----NDQTLFELKIPSTLA-----PPMDPSVPIWIIIFG----- 148
Db 550 NEDNSLSILAKHNGFNROKQEVYLLPIVISDSGNPPLSSTLTIRVCGCSNDGVVQSCN 609
QY 149 -----VIFCIIIVAIALLILSGIWQRRRNKKEPSEVDDAEDKCNENMIT 191
Db 610 VEAYVLPGLSMGALIAILACIILLVIVVLF--VTLRRHKN-EPLIIKDEEDVRENIIR 666
QY 192 IEN 194
Db 667 YDD 669
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RESULT 8
US-08-188-228-54
; Sequence 54, Application US/08188228
; Patent No. 5597725
; GENERAL INFORMATION:
; APPLICANT: Suzuki, Shintaro
; TITLE OF INVENTION: CADHERIN MATERIALS AND METHODS
; NUMBER OF SEQUENCES: 62
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Borun
; STREET: 6300 Sears Tower, 233 S. Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/188,228
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/049,460
; FILING DATE: 19 APR 1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/872,643
; FILING DATE: 17 APR 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5597725and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 31340
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
```

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; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 54:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 793 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-188-228-54

Query Match      8.1%; Score 89.5; DB 1; Length 793;
Best Local Similarity 20.6%; Pred. No. 0.22;
Matches 50; Conservative 35; Mismatches 93; Indels 65; Gaps 10;

QY 13 HAEICQPGAENAFKVRLSIRLTALGDKAYAWDT-----NEEYLFKAMVAFSMRKVPN 63
Db 425 HTDLERQFNINADGKITLATPLDRELSVWHNIIATEIRNHSQISRVPVAIKVLDV-N 483
QY 64 REATEIS---HVLIC-----NVTQVSVFWVVTDPKSNH-----TLPAVEVQSAIRMNK 109
Db 484 DNAPEFASEYEAFLECGKPGQVIQTVSA-MDKDDPKNGHFFLYSLPEMNNPNFTIKK 542
QY 110 NRINNAPFL-----NDQTLFELKIPSTLA-----PPMDPSVPIWIIIFG----- 148
Db 543 NEDNSLSILAKHNGFNROKQEVYLLPIIISDSGNPPLSSTLTIRVCGCSNDGVVQSCN 602
QY 149 -----VIFCIIIVAIALLILSGIWQRRRNKKEPSEVDDAEDKCNENMIT 191
Db 603 VEAYVLPGLSMGALIAILACIILLVIVVLF--VTLRRHKN-EPLIIKDEEDVRENIIR 660
QY 192 IEN 194
Db 661 YDD 663

RESULT 9
US-08-332-643-48
; Sequence 48, Application US/08332643
; Patent No. 5639634
; GENERAL INFORMATION:
; APPLICANT: Suzuki, Shintaro
; TITLE OF INVENTION: CADHERIN MATERIALS AND METHODS
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Bicknell
; STREET: Two First National Plaza, 20 South Clark
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/332,643
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/872,643
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5639634and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/30795
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 346-5750
; TELEFAX: (312) 984-9740
; TELE: 25-3856
; INFORMATION FOR SEQ ID NO: 48:
; SEQUENCE CHARACTERISTICS:
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US-07-946-497-7

Query Match 8.0%; Score 88; DB 1; Length 363;
Best Local Similarity 21.6%; Pred. No. 0.11;
Matches 24; Conservative 23; Mismatches 30; Indels 34; Gaps 3;

Qy 128 IPSTLAPPDPSVPIWIIIFGVIFCIIVAIALLILSGIWQRR-----PLDMKGGI 171

Db 256 VTTTSGPMRRPQIPEWLI---LASLLALILAVCIAVNSRRRCGQKKLVINGNGTV 312

Qy 172 KNKEPSEVDDAEDKCNMTIENGIPSD-----PLDMKGGI 207

Db 313 EDRKPSSELNGEASKSQEMVHLVNKEPSETPDQCMTADETRNLSQVDMKIGV 363

RESULT 12

US-08-483-322-7
; Sequence 7, Application US/08483322
; Patent No. 5760178

; GENERAL INFORMATION:

; APPLICANT: HERRLICH, Peter
; APPLICANT: PONTA, Helmut
; APPLICANT: GUENTHERT, Ursula
; APPLICANT: MATZKU, Siegfried
; APPLICANT: WENZL, Achim

; TITLE OF INVENTION: VARIANT CD44 SURFACE PROTEINS, DNA
; TITLE OF INVENTION: SEQUENCES CODING THESE, ANTIBODIES AGAINST THESE PROTEINS,
; TITLE OF INVENTION: AS WELL AS THEIR USE IN DIAGNOSIS AND THERAPY
; NUMBER OF SEQUENCES: 8

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington, D.C.
; COUNTRY: USA
; ZIP: 20007-5109

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/483,322

; FILING DATE: 07-JUN-1995

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/946,497

; FILING DATE: 09-NOV-1992

; ATTORNEY/AGENT INFORMATION:

; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 16915/145

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (202)672-5300

; TELEFAX: (202)672-5399

; TELEX: 904136

; INFORMATION FOR SEQ ID NO: 7:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 363 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; IMMEDIATE SOURCE:

; CLONE: mCD44

US-08-483-322-7

Query Match 8.0%; Score 88; DB 1; Length 363;

Best Local Similarity 21.6%; Pred. No. 0.11;
Matches 24; Conservative 23; Mismatches 30; Indels 34; Gaps 3;

Qy 128 IPSTLAPPDPSVPIWIIIFGVIFCIIVAIALLILSGIWQRR-----PLDMKGGI 171

Db 256 VTTTSGPMRRPQIPEWLI---LASLLALILAVCIAVNSRRRCGQKKLVINGNGTV 312

Qy 172 KNKEPSEVDDAEDKCNMTIENGIPSD-----PLDMKGGI 207

Db 313 EDRKPSSELNGEASKSQEMVHLVNKEPSETPDQCMTADETRNLSQVDMKIGV 363

RESULT 13

US-08-478-882-7
; Sequence 7, Application US/08478882
; Patent No. 5885575

; GENERAL INFORMATION:

; APPLICANT: HERRLICH, Peter
; APPLICANT: PONTA, Helmut
; APPLICANT: GUENTHERT, Ursula
; APPLICANT: MATZKU, Siegfried
; APPLICANT: WENZL, Achim

; TITLE OF INVENTION: VARIANT CD44 SURFACE PROTEINS, DNA

; TITLE OF INVENTION: SEQUENCES CODING THESE, ANTIBODIES AGAINST THESE PROTEINS,
; TITLE OF INVENTION: AS WELL AS THEIR USE IN DIAGNOSIS AND THERAPY
; NUMBER OF SEQUENCES: 8

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington, D.C.
; COUNTRY: USA
; ZIP: 20007-5109

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/478,882

; FILING DATE:

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/07/946,497

; FILING DATE: 19921109

; ATTORNEY/AGENT INFORMATION:

; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 16915/145

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (202)672-5300

; TELEFAX: (202)672-5399

; TELEX: 904136

; INFORMATION FOR SEQ ID NO: 7:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 363 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; IMMEDIATE SOURCE:

; CLONE: mCD44

US-08-478-882-7

Query Match 8.0%; Score 88; DB 2; Length 363;

Best Local Similarity 21.6%; Pred. No. 0.11;
Matches 24; Conservative 23; Mismatches 30; Indels 34; Gaps 3;

Qy 128 IPSTLAPPDPSVPIWIIIFGVIFCIIVAIALLILSGIWQRR-----PLDMKGGI 171

Db 256 VTTTSGPMRRPQIPEWLI---LASLLALILAVCIAVNSRRRCGQKKLVINGNGTV 312

Qy 172 KNKEPSEVDDAEDKCNMTIENGIPSD-----PLDMKGGI 207

Db 313 EDRKPSSELNGEASKSQEMVHLVNKEPSETPDQCMTADETRNLSQVDMKIGV 363

RESULT 14

US-07-946-497-2

; Sequence 2, Application US/07946497
; Patent No. 5506119

; GENERAL INFORMATION:

; APPLICANT: HERRLICH, Peter
; APPLICANT: PONTA, Helmut

APPLICANT: GUENTHER, Ursula
APPLICANT: MATZKU, Siegfried
APPLICANT: WENZL, Achim
TITLE OF INVENTION: VARIANT CD44 SURFACE PROTEINS, DNA
TITLE OF INVENTION: SEQUENCES CODING THESE, ANTIBODIES AGAINST THESE PROTEINS,
TITLE OF INVENTION: AS WELL AS THEIR USE IN DIAGNOSIS AND THERAPY
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington, D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/946,497
FILING DATE: 19921109
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 16915/145
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 503 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-946-497-2

Query Match 7.8%; Score 86; DB 1; Length 503;
Best Local Similarity 20.7%; Pred. No. 0.29;
Matches 23; Conservative 24; Mismatches 30; Indels 34; Gaps 3;
Qy 128 IPSTLAPPMDPSVPIWIIIFGVIFCIIVAIALLILSGIWQRR-----171
Db 396 VTTTSGPARRPQIPEWLI---LASLLALALILAVCIANSRRRCQKKLVINSNGTV 452
Qy 172 KNKEPSEVDDAEDKCNMITIENGIPSD-----PLDMKGGI 207
Db 453 EDRKPESELNGEASKSQEMVHLVNKEPTETPDQFMTADETRNLQSVDMKIGV 503

RESULT 15
US-08-483-322-2
Sequence 2, Application US/08483322
Patent No. 5760178
GENERAL INFORMATION:
APPLICANT: HERRLICH, Peter
APPLICANT: PONTA, Helmut
APPLICANT: GUENTHER, Ursula
APPLICANT: MATZKU, Siegfried
APPLICANT: WENZL, Achim
TITLE OF INVENTION: VARIANT CD44 SURFACE PROTEINS, DNA
TITLE OF INVENTION: SEQUENCES CODING THESE, ANTIBODIES AGAINST THESE PROTEINS,
TITLE OF INVENTION: AS WELL AS THEIR USE IN DIAGNOSIS AND THERAPY
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington, D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,322
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/946,497
FILING DATE: 09-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 16915/145
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 503 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-483-322-2
Query Match 7.8%; Score 86; DB 1; Length 503;
Best Local Similarity 20.7%; Pred. No. 0.29;
Matches 23; Conservative 24; Mismatches 30; Indels 34; Gaps 3;
Qy 128 IPSTLAPPMDPSVPIWIIIFGVIFCIIVAIALLILSGIWQRR-----171
Db 396 VTTTSGPARRPQIPEWLI---LASLLALALILAVCIANSRRRCQKKLVINSNGTV 452
Qy 172 KNKEPSEVDDAEDKCNMITIENGIPSD-----PLDMKGGI 207
Db 453 EDRKPESELNGEASKSQEMVHLVNKEPTETPDQFMTADETRNLQSVDMKIGV 503

Search completed: March 31, 2004, 12:07:51
Job time : 24 secs

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OM protein - protein search, using sw model

Run on: March 31, 2004, 12:06:50 ; Search time 42 Seconds
(without alignments)
1320.769 Million cell updates/sec

Title: US-09-989-724-387
Perfect score: 1102
Sequence: 1 MLWLLFLVTAIHAELCPG.....ENGIPSDPLDMKGILMMP 212

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Searched: 1065169 seqs, 261661801 residues

Total number of hits satisfying chosen parameters: 1065169

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1102	100.0	212	9 US-09-989-723-387	Sequence 387, App
3	1102	100.0	212	9 US-09-989-279-387	Sequence 387, App
4	1102	100.0	212	9 US-09-989-727-387	Sequence 387, App
5	1102	100.0	212	9 US-09-989-731-387	Sequence 387, App
6	1102	100.0	212	9 US-09-989-732-387	Sequence 387, App
7	1102	100.0	212	9 US-09-991-073-387	Sequence 387, App
8	1102	100.0	212	9 US-09-990-442-387	Sequence 387, App
9	1102	100.0	212	9 US-09-991-163-387	Sequence 387, App
10	1102	100.0	212	9 US-09-993-604-387	Sequence 387, App
11	1102	100.0	212	9 US-09-990-456-387	Sequence 387, App
12	1102	100.0	212	9 US-09-989-721-387	Sequence 387, App
13	1102	100.0	212	9 US-09-992-598-387	Sequence 387, App
14	1102	100.0	212	9 US-09-989-293A-387	Sequence 387, App
15	1102	100.0	212	9 US-09-989-735-387	Sequence 387, App

16	1102	100.0	212	9 US-09-990-444-387	Sequence 387, App
17	1102	100.0	212	9 US-09-991-181-387	Sequence 387, App
18	1102	100.0	212	9 US-09-989-730-387	Sequence 387, App
19	1102	100.0	212	9 US-09-990-436-387	Sequence 387, App
20	1102	100.0	212	9 US-09-993-687-387	Sequence 387, App
21	1102	100.0	212	10 US-09-989-734-387	Sequence 387, App
22	1102	100.0	212	10 US-09-997-653-387	Sequence 387, App
23	1102	100.0	212	10 US-09-993-667-387	Sequence 387, App
24	1102	100.0	212	10 US-09-997-428-387	Sequence 387, App
25	1102	100.0	212	10 US-09-997-666-387	Sequence 387, App
26	1102	100.0	212	10 US-09-990-438-387	Sequence 387, App
27	1102	100.0	212	10 US-09-990-562-387	Sequence 387, App
28	1102	100.0	212	10 US-09-990-711-387	Sequence 387, App
29	1102	100.0	212	10 US-09-989-726-387	Sequence 387, App
30	1102	100.0	212	10 US-09-998-156-387	Sequence 387, App
31	1102	100.0	212	10 US-09-990-437-387	Sequence 387, App
32	1102	100.0	212	10 US-09-991-157-387	Sequence 387, App
33	1102	100.0	212	10 US-09-997-514-387	Sequence 387, App
34	1102	100.0	212	10 US-09-997-573-387	Sequence 387, App
35	1102	100.0	212	10 US-09-991-172-387	Sequence 387, App
36	1102	100.0	212	10 US-09-990-726-387	Sequence 387, App
37	1102	100.0	212	10 US-09-997-559-387	Sequence 387, App
38	1102	100.0	212	10 US-09-997-601-387	Sequence 387, App
39	1102	100.0	212	10 US-09-990-443-387	Sequence 387, App
40	1102	100.0	212	10 US-09-991-854-387	Sequence 387, App
41	1102	100.0	212	10 US-09-997-628-387	Sequence 387, App
42	1102	100.0	212	10 US-09-997-683-387	Sequence 387, App
43	1102	100.0	212	10 US-09-989-729A-387	Sequence 387, App
44	1102	100.0	212	10 US-09-997-349-387	Sequence 387, App
45	1102	100.0	212	10 US-09-997-440-387	Sequence 387, App

ALIGNMENTS

RESULT 1

US-09-989-722-387
; Sequence 387, Application US/09989722
; Patent No. US20020072067A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C63
; CURRENT APPLICATION NUMBER: US/09/989,722
; CURRENT FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17

; PRIOR APPLICATION NUMBER: 60/091360
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/091478
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091544
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; PRIOR APPLICATION NUMBER: 60/091633
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 1102; DB 9; Length 212;
Best Local Similarity 100.0%; Pred. No. 3.5e-113;
Matches 212; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLWLLFVLTAIHAELCPGAENAFKVRISIRLTALGDKAYAWDTNEEYLPKAMVAFSMRK 60
Db 1 MLWLLFVLTAIHAELCPGAENAFKVRISIRLTALGDKAYAWDTNEEYLPKAMVAFSMRK 60
Qy 61 VPNREATEISHVLLCNVTQVSVFVVTDPFSKNHTLPAVEVQSAIRMNKRINNAFFLND 120
Db 61 VPNREATEISHVLLCNVTQVSVFVVTDPFSKNHTLPAVEVQSAIRMNKRINNAFFLND 120
Qy 121 QTLEFLKIPSTLAPPMDSVPFIWIIIFGVIFCIIIVAIALLILSGIWQRRRKNKEPSEVD 180
Db 121 QTLEFLKIPSTLAPPMDSVPFIWIIIFGVIFCIIIVAIALLILSGIWQRRRKNKEPSEVD 180
Qy 181 DAEDKCENMTIENGIPSDPLDMKGGILMMP 212
Db 181 DAEDKCENMTIENGIPSDPLDMKGGILMMP 212

RESULT 2

US-09-989-723-387
; Sequence 387, Application US/09989723
; Patent No. US20020072092A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
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; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C62
; CURRENT APPLICATION NUMBER: US/09/989,723

; CURRENT FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/049787
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; PRIOR APPLICATION NUMBER: 60/090863
; PRIOR FILING DATE: 1998-06-26
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; PRIOR APPLICATION NUMBER: 60/091626
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091633
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 1102; DB 9; Length 212;
Best Local Similarity 100.0%; Pred. No. 3.5e-113;
Matches 212; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLMLLPPLVTAIHAELCQPGAENAFKVRLSIRTALGDKAYAWDTNEEYLPKAMVAFSMRK 60
Db 1 MLMLLPPLVTAIHAELCQPGAENAFKVRLSIRTALGDKAYAWDTNEEYLPKAMVAFSMRK 60

Qy 61 VPNREATEISHVLLCNVTQVSFWFVTDPSKNHTLPAVEVQS AIRMKNRINNAFFLND 120
Db 61 VPNREATEISHVLLCNVTQVSFWFVTDPSKNHTLPAVEVQS AIRMKNRINNAFFLND 120

Qy 121 QTLFLKIPSTLAPPMDPSVPIWIIIFGVIFPCIIIVAIALLILSGIWQRRKNKEPSEVD 180
Db 121 QTLFLKIPSTLAPPMDPSVPIWIIIFGVIFPCIIIVAIALLILSGIWQRRKNKEPSEVD 180

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Db 181 DAEDKCNMITIENGIPSDPLDMKGGILMMPMS 212

RESULT 3

US-09-989-279-387
; Sequence 387, Application US/09989279
; Patent No. US20020072496A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary B.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas P.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.

APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730P1C56
CURRENT APPLICATION NUMBER: US/09/989,279
PRIOR FILING DATE: 2001-11-19
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066770
PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/075945
PRIOR FILING DATE: 1998-02-25
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/083322
PRIOR FILING DATE: 1998-04-28
PRIOR APPLICATION NUMBER: 60/084600
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/087106
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; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 1102; DB 9; Length 212;
Best Local Similarity 100.0%; Pred. No. 3.5e-113;
Matches 212; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLWLLFPLVTAIHAELCQPGAENAFKVRLSIRTALGDKAYAWDTNBEYLFKAMVAFSMRK 60
Db 1 MLWLLFPLVTAIHAELCQPGAENAFKVRLSIRTALGDKAYAWDTNBEYLFKAMVAFSMRK 60
Qy 61 VPNREATEISHVLLCNVTQVSFWFVVTDPKSNHTLPAVEVQSAIRMNKNRINNAPFLND 120
Db 61 VPNREATEISHVLLCNVTQVSFWFVVTDPKSNHTLPAVEVQSAIRMNKNRINNAPFLND 120
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Db 121 QTLEFLKIPSTLAPMDPSVPIWIIIFGVIPCIIVAIALLILSGIWQRRRKNKEPSEVD 180
Qy 181 DAEDKCNMITIENGIPSDPLDMKGGILMMP 212
Db 181 DAEDKCNMITIENGIPSDPLDMKGGILMMP 212

RESULT 4

US-09-989-727-387
; Sequence 387, Application US/09989727
; Patent No. US20020072497A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
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; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730PIC65
; CURRENT APPLICATION NUMBER: US/09/989,727
; CURRENT FILING DATE: 2001-11-19
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; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 1102; DB 9; Length 212;
Best Local Similarity 100.0%; Pred. No. 3.5e-113;
Matches 212; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db	61	VPNREATEISHVLLCNVTQVRSFVVTDPSPKNHTLPAVEVQSAIRMNKNRINNNAFFLND	120
Qy	121	QTLFELKIPSTLAPMDPSVPIWIIIFGVIFCIIIVATAILLISGIWQRKKNKEPSEVD	180
Db	121	QTLFELKIPSTLAPMDPSVPIWIIIFGVIFCIIIVATAILLISGIWQRKKNKEPSEVD	180
Qy	181	DAEDKCNMITIENGIPSDPLDMKGGILMMP	212
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RESULT 5
US-09-989-731-387
; Sequence 387, Application US/09989731
; Patent No. US20020103125A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
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APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730PIC70
CURRENT APPLICATION NUMBER: US/09/989,731
CURRENT FILING DATE: 2001-11-20
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; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 1102; DB 9; Length 212;

Best Local Similarity 100.0%; Pred. No. 3.5e-113;

Matches 212; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 61 VPKREATEISHVLLCNVTQRVSFVVTDPKSNHTLPAVEVQSAIRMNKRNINNAFFLND 120
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Db 121 QTLFELKIPSTLAPPMDPSVPIWIIIFGVIFCIIVAIALLILSGIWQRRRNKEPSEVD 180
Qy 181 DAEDKCNMITIENGIPSDPLDMKGILMPS 212
Db 181 DAEDKCNMITIENGIPSDPLDMKGILMPS 212

RESULT 6

US-09-989-732-387

; Sequence 387, Application US/09989732

; Patent No. US20020123463A1

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi J.

; APPLICANT: Baker, Kevin P.

; APPLICANT: Botstein, David

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; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C57
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; PRIOR APPLICATION NUMBER: 60/091633
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 1102; DB 9; Length 212;

Best Local Similarity 100.0%; Pred. No. 3.5e-113;

Matches 212; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db	1	MLWLLFFLVTAIHAELCQGAENAFKVRISRTALGDKAYAWDTNEEYLFKAMVAFSMRK	60
Qy	61	VPNREATEISHVLLCNVTQVSFWFVVTDPKSNHTLPAVEVQSAIRMNKNRINNAFFLND	120
Db	61	VPNREATEISHVLLCNVTQVSFWFVVTDPKSNHTLPAVEVQSAIRMNKNRINNAFFLND	120
Qy	121	QTLFLKIPSTLAPPMDSVPFIWIIIFGVIFCIIIVAIALLISGIWQRRRKNKPSSEVD	180
Db	121	QTLFLKIPSTLAPPMDSVPFIWIIIFGVIFCIIIVAIALLISGIWQRRRKNKPSSEVD	180
Qy	181	DAEDKCNMTIENGIPSDPLDMKGGILMPS	212
Db	181	DAEDKCNMTIENGIPSDPLDMKGGILMPS	212

RESULT 7

US-09-991-073-387

; Sequence 387, Application US/09991073

; Patent No. US20020127576A1

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi J.

; APPLICANT: Baker, Kevin P.

; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730PIC15
; CURRENT APPLICATION NUMBER: US/09/991,073
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
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; PRIOR FILING DATE: 1997-11-12
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; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
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; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 1102; DB 9; Length 212;
Best Local Similarity 100.0%; Pred. No. 3.5e-113;
Matches 212; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLWLLFFLVTAIHAELCQGAENAPKVRLSIRTAIGDKAYAWDTNTEEYLFKAMVAFSMRK 60
Db 1 MLWLLFFLVTAIHAELCQGAENAPKVRLSIRTAIGDKAYAWDTNTEEYLFKAMVAFSMRK 60

QY 61 VFNREATEISHVLLCNVTQVSFWFVVTDPKSNHTLPAVEQSAIRMNKNRINNAFFLND 120
Db 61 VFNREATEISHVLLCNVTQVSFWFVVTDPKSNHTLPAVEQSAIRMNKNRINNAFFLND 120

QY 121 QTFLEFLKIPSTLAPPMDPSVPIWIIIFGVIFCIIIVAIALLISGIWQRRRNKKEPSEVD 180
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QY 181 DAEDKCNMTIENGIPSDPLDKGGLMMP 212
Db 181 DAEDKCNMTIENGIPSDPLDKGGLMMP 212

RESULT 8
US-09-990-442-387
; Sequence 387, Application US/09990442

; Patent No. US20020132252A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
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; APPLICANT: Grimaldi, J. Christopher
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; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C8
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; PRIOR FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/049787
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; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 1102; DB 9; Length 212;
Best Local Similarity 100.0%; Pred. No. 3.5e-113;
Matches 212; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLWLLFFLVTAIHAELCQPGAENAFKRLSINTALGDKAYANDTNEEYLFKAMVAFSMRK 60
Db 1 MLWLLFFLVTAIHAELCQPGAENAFKRLSINTALGDKAYANDTNEEYLFKAMVAFSMRK 60
Qy 61 VPNREATEISHVLLCNVTQVSFWFVVTDPCKNHTLPAVEVQSAIRMNKRNINNAFFLND 120
Db 61 VPNREATEISHVLLCNVTQVSFWFVVTDPCKNHTLPAVEVQSAIRMNKRNINNAFFLND 120
Qy 121 QTFLEFLKIPSTLAPMDPSVPIWIIIFGVIFCIIIVAIALLISGIWQRRRKNEPSEVD 180
Db 121 QTFLEFLKIPSTLAPMDPSVPIWIIIFGVIFCIIIVAIALLISGIWQRRRKNEPSEVD 180
Qy 181 DAEDKCENMITIENGIPSDPLDMKGGILMPS 212
Db 181 DAEDKCENMITIENGIPSDPLDMKGGILMPS 212

RESULT 9

US-09-991-163-387
; Sequence 387, Application US/09991163
; Patent No. US20020132253A1

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
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; APPLICANT: Godowski, Paul J.
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; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
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; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

; TITLE OF INVENTION: Acids Encoding the Same

; FILE REFERENCE: P2730P1C17

; CURRENT FILING DATE: 2001-11-14

; CURRENT FILING DATE: 2001-11-14

; PRIOR APPLICATION NUMBER: 60/049787

; PRIOR APPLICATION NUMBER: 60/062250

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Query Match 100.0%; Score 1102; DB 9; Length 212;
Best Local Similarity 100.0%; Pred. No. 3.5e-113;
Matches 212; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
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; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
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?	PRIOR FILING DATE:	1998-07-07

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Best Local Similarity	100.0%;	Pred. No. 3.5e-113;

Best local similarity 100.0%, P.E.D. NO. 3:30 115)
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; APPLICANT: Botstein, David
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; APPLICANT: Eaton, Dan L.
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; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
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; PRIOR APPLICATION NUMBER: 60/090542
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090557
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090676
; PRIOR FILING DATE: 1998-06-25
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; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091633
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 1102; DB 9; Length 212;
Best Local Similarity 100.0%; Pred. No. 3.5e-113;
Matches 212; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLWLFLVTAIHAEICQPGAENAPKVRLSIRTALGDKAYADTNEEYLPKAMVAFSMRK 60
Db 1 MLWLFLVTAIHAEICQPGAENAPKVRLSIRTALGDKAYADTNEEYLPKAMVAFSMRK 60
Qy 61 VPNREATEISHVLLCNVTQVRVSFWFVVTDPKQHTLPAVEVQSAIRMNKNRINNAPFLND 120
Db 61 VPNREATEISHVLLCNVTQVRVSFWFVVTDPKQHTLPAVEVQSAIRMNKNRINNAPFLND 120
Qy 121 QTLFLKIPSTLAPMDPSVPIWIIIFGVIFCIIIVAIALLILSGIWQRRKNKEPSEVD 180
Db 121 QTLFLKIPSTLAPMDPSVPIWIIIFGVIFCIIIVAIALLILSGIWQRRKNKEPSEVD 180
Qy 181 DAEDKCNMITIENGIPSDPLDMKGGILMMPMS 212
Db 181 DAEDKCNMITIENGIPSDPLDMKGGILMMPMS 212

RESULT 12

US-09-989-721-387
; Sequence 387, Application US/09989721
; Patent No. US20020142961A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730PLC55
; CURRENT APPLICATION NUMBER: US/09/989,721
; PRIOR FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
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; PRIOR FILING DATE: 1997-11-12
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; PRIOR FILING DATE: 1997-11-24
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; PRIOR APPLICATION NUMBER: 60/087106
; PRIOR FILING DATE: 1998-05-28
; PRIOR APPLICATION NUMBER: 60/087607
; PRIOR FILING DATE: 1998-06-02

Query Match 100.0%; Score 1102; DB 9; Length 212;
Best Local Similarity 100.0%; Pred. No. 3.5e-113;
Matches 212; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLWLLFFLVTAIHAELCQCAENAFKVRISRTALGDKAYAWDTNEEYLFKAMVAFSMRK 60
Db 1 MLWLLFFLVTAIHAELCQCAENAFKVRISRTALGDKAYAWDTNEEYLFKAMVAFSMRK 60

Qy 61 VPNREATEISHVLLCNVTQVSFWFVVTDSKNHTLPAVEVQSAIRMNKNRINNAFFLND 120
Db 61 VPNREATEISHVLLCNVTQVSFWFVVTDSKNHTLPAVEVQSAIRMNKNRINNAFFLND 120

Qy 121 QTLFLKIPSTLAPPMPSVPIWIIIFGVIFCIIIVAIALLILSGIWQRKKKEPSEVD 180
Db 121 QTLFLKIPSTLAPPMPSVPIWIIIFGVIFCIIIVAIALLILSGIWQRKKKEPSEVD 180

Qy 181 DAEDKCNMTIENGIPSDPLDMKGGILMMPS 212
Db 181 DAEDKCNMTIENGIPSDPLDMKGGILMMPS 212

RESULT 13

US-09-992-598-387
; Sequence 387, Application US/09992598
; Patent No. US20020160384A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
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; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C20
; CURRENT APPLICATION NUMBER: US/09/992,598
; CURRENT FILING DATE: 2001-11-14
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; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091978

; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 1102; DB 9; Length 212;
Best Local Similarity 100.0%; Pred. No. 3.5e-113;
Matches 212; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLWLLFFLVTAIHAELCQPGAENAFKVRSLRTALGDKAYAWDTNEEYLFKAMVAFSMRK 60
Db 1 MLWLLFFLVTAIHAELCQPGAENAFKVRSLRTALGDKAYAWDTNEEYLFKAMVAFSMRK 60

QY 61 VPRNREATEISHVLLCNVTQVSFVFVVTDPSPKNTLPAVEVQSAIRMNKNRINNNAFFLND 120
Db 61 VPRNREATEISHVLLCNVTQVSFVFVVTDPSPKNTLPAVEVQSAIRMNKNRINNNAFFLND 120

QY 121 QTLFPLKIPSTLAPPMDPSVPIWIIIFGVIFCIIVAIALLILSGIWQRRRNKKEPSEVD 180
Db 121 QTLFPLKIPSTLAPPMDPSVPIWIIIFGVIFCIIVAIALLILSGIWQRRRNKKEPSEVD 180

QY 181 DAEDKCNMITIENGIPSDPLDMKGILMPS 212
Db 181 DAEDKCNMITIENGIPSDPLDMKGILMPS 212

RESULT 14
US-09-989-293A-387
; Sequence 387, Application US/09989293A
; Patent No. US20020177164A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary B.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730PIC66
; CURRENT APPLICATION NUMBER: US/09/989,293A
; CURRENT FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066770
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/075945
; PRIOR FILING DATE: 1998-02-25


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; PRIOR APPLICATION NUMBER: 60/091626
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091633
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
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; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match          100.0%; Score 1102; DB 9; Length 212;
Best Local Similarity 100.0%; Pred. No. 3.5e-113;
Matches 212; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLWLLFFLVTAIHAEICQPGAENAFKVRLSIRLTALGDKAYAWDTNTEYLFKAMVAPSMRK 60
DQ 1 MLWLLFFLVTAIHAEICQPGAENAFKVRLSIRLTALGDKAYAWDTNTEYLFKAMVAPSMRK 60
QY 61 VPREATEISHVLLCNVTQVSFVFVVTDPKKNHTLPAVEVQSAIRMNKNRINNNAFFLND 120
DQ 61 VPREATEISHVLLCNVTQVSFVFVVTDPKKNHTLPAVEVQSAIRMNKNRINNNAFFLND 120
QY 121 QTFLEFLKIPSTLAPPMDPSVPIWIIIFGVIFCIIVAIALLILSGIWORRRKNKEPSEVD 180
DQ 121 QTFLEFLKIPSTLAPPMDPSVPIWIIIFGVIFCIIVAIALLILSGIWORRRKNKEPSEVD 180
QY 181 DAEDKCNMITIENGIPSDPLDMKGILMMP 212
DQ 181 DAEDKCNMITIENGIPSDPLDMKGILMMP 212

RESULT 15
US-09-989-735-387
; Sequence 387, Application US/09989735
; Publication No. US20020193299A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730PIC61
; CURRENT APPLICATION NUMBER: US/09/989,735
; CURRENT FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
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; PRIOR APPLICATION NUMBER: 60/066770
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;	PRIOR FILING DATE: 1998-06-26
;	PRIOR APPLICATION NUMBER: 60/091360
;	PRIOR FILING DATE: 1998-07-01
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; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

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Query Match 100.0%: Score 1102: DB 9: Length 212:

Query Match 100.0%; Score 11v2; DB 3;
Best Local Similarity 100.0%; Pred. No. 3.5e-113;

Best local similarity 100.0%, PEG: NO: 3:30-113,
Matches 212: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Search completed: March 31, 2004. 12:12:28

Job time : 43 secs

GenCore version 5.1.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model
Run on: April 3, 2004, 23:26:59 ; Search time 3771 Seconds
(without alignments)
2436.681 Million cell updates/sec

Title: US-09-989-724-387
Perfect score: 1102
Sequence: 1 MWLLFVLVTAHAEIQCQPG.....ENGIPSDPLDKGGLMMP 212

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1102	100.0	1346	6	AR252633 Sequence
2	1102	100.0	1346	6	AX403499 Sequence
3	1102	100.0	1346	6	AX464348 Sequence
4	1102	100.0	1346	9	AY359060 Homo sapi
5	1089	98.8	666	6	AX083382 Sequence
6	1089	98.8	1345	9	AF229179 Homo sapi
7	1089	98.8	1347	6	AX083392 Sequence
8	1089	98.8	1377	9	BC050606 Homo sapi
9	1089	98.8	1440	9	BC015099 Homo sapi
10	1089	98.8	1605	9	BC014317 Homo sapi
11	1086	98.5	1401	6	BD083420 Secreted
12	1082	98.2	1447	6	BD205644 97 human
13	1064	96.6	848	6	AR177334 Sequence
14	1064	96.6	848	6	BD247957 5' EST f
15	1064	96.6	848	6	AR340701 Sequence
16	1064	96.6	848	6	AR412373 Sequence
17	1064	96.6	848	6	AX884142 Sequence
18	1064	96.6	848	6	BD023757 Sequence
19	1064	96.6	848	6	BD073618 5'EST of
20	1064	96.6	848	6	BD075896 5' EST of
21	1064	96.6	848	6	BD076074 5' EST of
22	1064	96.6	848	6	BD076775 5' BST of
23	1064	96.6	848	6	BD077436 5'EST of
24	1064	96.6	848	6	BD077737 5'EST of
25	1064	96.6	848	6	BD085880 Blongatio
26	1064	96.6	848	6	BD107926 EST and e
27	1064	96.6	848	6	BD131408 CDNA enco
28	1064	96.6	848	6	BD139270 Extended
29	1064	96.6	848	6	BD203799 5'EST and
30	1062	96.4	1356	6	BD135300 110 human
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33	924	83.8	1181	10	AF178086 Rattus no
34	694	63.0	439	6	BD077452 5'EST of
35	674	61.2	462	6	BD058424 Secreted
36	488	44.3	1131	5	BC058203 Xenopus l
37	387.5	35.2	1879	5	BC053284 Danio rer
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39	376	34.1	2415	6	BD274685 Angiotens
40	376	34.1	2415	6	E43987 ACE-analogo
41	376	34.1	2415	6	AR382342 Sequence
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ALIGNMENTS

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LOCUS AR252633 1346 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 386 from patent US 6478825.
ACCESSION AR252633
VERSION AR252633.1 GI:27300541
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1346)
AUTHORS Winterbottom,J.M., Shimp,L., Boyce,T.M. and Kaes,D.
TITLE Implant, method of making same and use of the implant for the
treatment of bone defects
JOURNAL Patent: US 6478825-A 386 12-NOV-2002;
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source Location/Qualifiers
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Pred. No.: 1102.00 Matches: 212
Score: 100.00% Conservative: 0
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Best Local Similarity: 100.00% Indels: 0
Query Match: 100.00% Gaps: 0
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Qy 101 ValGlnSerAlaIleArgMetAsnLysAsnArgIleAsnAsnAlaPhePheLeuAsnAsp 120
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LOCUS AX403499 1346 bp DNA linear PAT 14-JUN-2002
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ACCESSION AX403499
VERSION AX403499.1 GI:21436987
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
Ashkenazi,A.J., Baker,K.P., Botstein,D., Desnovers,L., Eaton,D.,
Ferrara,N., Gerber,H., Gerritsen,M., Goddard,A., Godowski,P.,
Grimaldi,C.J., Gurney,A.L., Kljavin,I., Napiet,M.A., Pan,J.,
Paoni,N.F., Roy,M., Stewart,T.A., Tumas,D., Watanabe,C.K.,
Williams,P., Wood,W.I. and Zhang,Z.
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding
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JOURNAL Patent: WO 0073454-A 386 07-DEC-2000;
Genentech Inc. (US)
FEATURES
source Location/Qualifiers
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Percent Similarity: 100.00% Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
Query Match: 100.00% Gaps: 0
DB: 6

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Qy 21 AlaGluAsnAlaPheLysValArgLeuSerIleArgThrAlaLeuGlyAspLysAlaTyr 40
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DEFINITION Sequence 481 from Patent WO0140466.
ACCESSION AX464348
VERSION AX464348.1 GI:21899190
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
REFERENCE
AUTHORS Baker, K.P., Beresini, M., Deforge, L., Desnoyers, L., Filvaroff, E.,
Gao, W.Q., Gerritsen, M.E., Goddard, A., Godowski, P.J., Gurney, A.L.,
Sherwood, S., Smith, V., Stewart, T.A., Tumas, D., Watanabe, C.K.,
Wood, W.L. and Zhang, Z.
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding
same
JOURNAL Patent: WO 0140466-A 481 07-JUN-2001;
Genentech Inc. (US)
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1. .1346
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Qy 41 AlaTrpAspThrAsnGluGluTyrLeuPheLysAlaMetValAlaPheSerMetArgLys 60
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DEFINITION Homo sapiens clone DNA61873 NX-17 (UNQ678) mRNA, complete cds.
ACCESSION AY359060
VERSION AY359060.1 GI:37183237
KEYWORDS FLI CDNA.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1346)
REFERENCE
AUTHORS Clark, H.F., Gurney, A.L., Abaya, E., Baker, K., Baldwin, D., Brush, J.,
Chen, J., Chow, B., Chui, C., Crowley, C., Currell, B., Deuel, B.,
Dowd, P., Eaton, D., Foster, J., Grimaldi, C., Gu, Q., Hass, P.E.,
Heldens, S., Huang, A., Kim, H.S., Klinowski, L., Jin, Y., Johnson, S.,
Lee, J., Lewis, L., Liao, D., Mark, M., Robbie, E., Sanchez, C.,
Schoenfeld, J., Seshagiri, S., Simmons, L., Singh, J., Smith, V.,
Stinson, J., Vagts, A., Vanden, R., Watanabe, C., Wieand, D., Woods, K.,
Xie, M.H., Yansura, D., Yi, S., Yu, G., Yuan, J., Zhang, M., Zhang, Z.,
Goddard, A., Wood, W.I. and Godowski, P.
TITLE The Secreted Protein Discovery Initiative (SPDI), a Large-Scale
Effort to Identify Novel Human Secreted and Transmembrane Proteins:
A Bioinformatics Assessment
JOURNAL Genome Res. 13 (10), 2265-2270 (2003)
PUBMED 12975309
REFERENCE 2 (bases 1 to 1346)
AUTHORS Clark, H.F.
TITLE Direct Submission
JOURNAL Submitted (01-AUG-2003) Department of Bioinformatics, Genentech,
Inc., 1 DNA Way, South San Francisco, CA 94080, USA
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Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-09-989-724-387 (1-212) x AY359060 (1-1346)

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Qy 1 MetLeuTrpLeuLeuPheLeuValThrAlaIleHisAlaGluLeuCysGlnProGly 20
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Db 7 ATGTTGGTGGTCTCTTTTCTGGTGACTGCCATTTCATGCTGAACCTCTGTCAACCCAGGT 66

Qy 21 AlaGluAsnAlaPheLysValArgLeuSerIleArgThrAlaLeuGlyAspLysAlaTyr 40
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Db 67 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 126

Qy 41 AlaTrpAspThrAsnGluGluTyrLeuPheLysAlaMetValAlaPheSerMetArgLys 60
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Db 127 GCCTGGGATACCAATGAAGATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA 186

Qy 61 ValProAsnArgGluAlaThrGluIleSerHisValLeuLeuCysAsnValThrGlnArg 80
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Db 187 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAAACCCAGAGG 246

Qy 81 ValSerPheTrpPheValValThrAspProSerLysAsnHisThrLeuProAlaValGlu 100
    |||||
Db 247 GTATCAATCTGGTTTGTGGTTACAGACCTTCAAAAAATCACAACCCCTTCTCTGTGTTGAG 306

Qy 101 ValGlnSerAlaIleArgMetAsnLysAsnArgIleAsnAsnAlaPhePheLeuAsnAsp 120
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Db 307 GTGCAATCAGCCCATAGAATGAACAGAACCGGATCAACAATGCCCTTCTTCTTAAATGAC 366

Qy 121 GlnThrLeuGluPheLeuLysIleProSerThrLeuAlaProProMetAspProSerVal 140
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Db 367 CAAACTCTGGAATTTTAAAAATCCCTTCCACACTTGCACCCATGGACCCCATCTGTG 426

Qy 141 ProIleTrpIleIleIlePheGlyValIlePheCysIleIleIleValAlaIleAlaLeu 160
    |||||
Db 427 CCCATCTGGATTATTATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTTGCACTA 486

Qy 161 LeuIleLeuSerGlyIleTrpGlnArgArgLysAsnLysGluProSerGluValAsp 180
    |||||
Db 487 CTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAAGTGGAT 546

Qy 181 AspAlaGluAspLysCysGluAsnMetIleThrIleGluAsnGlyIleProSerAspPro 200
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Db 547 GACGCTGAAGATAAGTGTGAACAACATGATCACAATTTGAAAATGGCATCCCTCTGTATCC 606

Qy 201 LeuAspMetLysGlyGlyIleLeuMetMetProSer 212
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Db 607 CTGGACATGAAGGGGGGCATATTAAATGATGCCTTCA 642
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RESULT 5
AX083382
LOCUS AX083382 Sequence 74 from Patent WO0112660. 666 bp DNA linear PAT 28-FEB-2001
ACCESSION AX083382
VERSION AX083382.1 GI:13185219

KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
AUTHORS Kato, S. and Kimura, T.
TITLE Human proteins having hydrophobic domains and dnas encoding these proteins
JOURNAL Patent: WO 0112660-A 74 22-FEB-2001;
SAGAMI CHEMICAL RESEARCH CENTER (JP) ; Protegene Inc. (JP)

FEATURES
source
1. .666
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN

Alignment Scores:
Pred. No.: 3.46e-113 Length: 666
Score: 1089.00 Matches: 212
Percent Similarity: 99.53% Conservative: 0
Best Local Similarity: 99.53% Mismatches: 0
Query Match: 98.82% Indels: 1
DB: 6 Gaps: 0

US-09-989-724-387 (1-212) x AX083382 (1-666)

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Qy 1 MetLeuTrpLeuLeuPheLeuValThrAlaIleHisAlaGluLeuCysGlnProGly 20
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Db 1 ATGTTGGTGGTCTCTTTTCTGGTGACTGCCATTTCATGCTGAACCTCTGTCAACCCAGGT 60

Qy 21 AlaGluAsnAlaPheLysValArgLeuSerIleArgThrAlaLeuGlyAspLysAlaTyr 40
    |||||
Db 61 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 120

Qy 41 AlaTrpAspThrAsnGluGluTyrLeuPheLysAlaMetValAlaPheSerMetArgLys 60
    |||||
Db 121 GCCTGGGATACCAATGAAGATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA 180

Qy 61 ValProAsnArgGluAlaThrGluIleSerHisValLeuLeuCysAsnValThrGlnArg 80
    |||||
Db 181 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAAATGAC 240

Qy 81 ValSerPheTrpPheValValThrAspProSerLysAsnHisThrLeuProAlaValGlu 100
    |||||
Db 241 GTATCAATCTGGTTTGTGGTTACAGACCTTCAAAAAATCACAACCCCTTCTCTGTGTTGAG 300

Qy 101 ValGlnSerAlaIleArgMetAsnLysAsnArgIleAsnAsnAlaPhePheLeuAsnAsp 120
    |||||
Db 301 GTGCAATCAGCCCATAGAATGAACAGAACCGGATCAACAATGCCCTTCTTCTTAAATGAC 360

Qy 121 GlnThrLeuGluPheLeuLysIleProSerThrLeuAlaProProMetAspProSerVal 140
    |||||
Db 361 CAAACTCTGGAATTTTAAAAATCCCTTCCACACTTGCACCCATGGACCCCATCTGTG 420

Qy 141 ProIleTrpIleIleIlePheGlyValIlePheCysIleIleIleValAlaIleAlaLeu 160
    |||||
Db 421 CCCATCTGGATTATTATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTTGCACTA 480

Qy 161 LeuIleLeuSerGlyIleTrpGlnArgArgLysAsnLysGluProSerGluValAsp 180
    |||||
Db 481 CTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAAGTGGAT 540

Qy 181 AspAlaGluAspLysCysGluAsnMetIleThrIleGluAsnGlyIleProSerAspPro 200
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Db 541 GACGCTGAAGATAAGTGTGAACAACATGATCACAATTTGAAAATGGCATCCCTCTGTATCC 600

Qy 201 LeuAspMetLysGlyGlyIleLeuMetMetProSer 212
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Db 601 CTGGACATGAAGGGGGGCATATTAAATGATGCCTTCA 637
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RESULT 6

AX083382
LOCUS AX083382
DEFINITION Homo sapiens collectrin mRNA, complete cds.
ACCESSION AX083382
VERSION AX083382.1 GI:9957753

KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 1345)
AUTHORS Zhang, H., Wada, J., Hida, K., Tsuchiyama, Y., Hiragushi, K.,
Shikata, K., Wang, H., Lin, S., Kanwar, Y.S. and Makino, H.
TITLE Collectrin, a collecting duct-specific transmembrane glycoprotein,
is a novel homolog of ACE2 and is developmentally regulated in
embryonic kidneys

JOURNAL J. Biol. Chem. 276 (20), 17132-17139 (2001)
MEDLINE 21264468
PUBMED 11278314
REFERENCE 2 (bases 1 to 1345)
AUTHORS Zhang,H., Wada,J. and Makino,H.
TITLE Human kidney specific membrane protein (NX-17)
JOURNAL Unpublished
REFERENCE 3 (bases 1 to 1345)
AUTHORS Zhang,H., Wada,J. and Makino,H.
TITLE Direct Submission
JOURNAL Submitted (28-JAN-2000) Department of Medicine III, Okayama
University Medical School, 2-5-1 Shikata-cho, Okayama 700-8558,
Japan

FEATURES
source Location/Qualifiers
1. .1345
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
24. .692
/note="kidney-specific membrane protein NX-17; similar to
the Mus musculus and Rattus norvegicus products encoded by
GenBank Accession Numbers AF178085 and AF178086,
respectively"
/codon_start=1
/product="collectrin"
/protein_id="AAG09466.1"
/db_xref="GI:9957754"
/translation="MLWLFLVTAIHAELCQGAENAFKVRLSIRTAIGDKAYAWDT
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ORIGIN

Alignment Scores:
Pred. No.: 8.14e-113 Length: 1345
Score: 1089.00 Matches: 212
Percent Similarity: 99.53% Conservative: 0
Best Local Similarity: 99.53% Mismatches: 0
Query Match: 98.82% Indels: 1
DB: 9 Gaps: 0

US-09-989-724-387 (1-212) x AF229179 (1-1345)

Qy 1 MetLeuTrpLeuLeuPheLeuValThrAlaIleHisAlaGluLeuCysGlnProGly 20
Db 24 ATGTTGTGGCTGCTCTTTTCTGGTGACTGCCATTGCTGAACCTCTGTCAACAGGT 83
Qy 21 AlaGluAsnAlaPheLysValArgLeuSerIleArgThrAlaLeuGlyAspLysAlaTyr 40
Db 84 GCAGAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAGCATAT 143
Qy 41 AlaTrpAspThrAsnGluGluTyrLeuPheLysAlaMetValAlaPheSerMetArgLys 60
Db 144 GCCTGGGATACCAATGAAGAAATACCTCTTCAAGCGATGGTAGCTTCTCCATGAGAAA 203
Qy 61 ValProAsnArgGluAlaThrGluIleSerHisValLeuLeuLeuValThrGlnArg 80
Db 204 GTTCCCAACAGAGAGCAACAGAAATTTCCCATGTCTACTTTGCAATGTACCCAGAG 263
Qy 81 ValSerPheTrpPheValValThrAspProSerLysAsnHisThrLeuProAlaValGlu 100
Db 264 GTATCATCTCTGTTGTGTTACAGACCTTCAAAAATCAACACCTTCTCTGCTTTGAA 323
Qy 101 ValGlnSerAlaIleArgMetAsnLysAsnArgIleAsnAsnAlaPhePheLeuAsnAsp 120
Db 324 GTGCAATCAGCCATAAGAAATGAACAAGAACCGGATCAACATGCGCTTCTTTAAATGAC 383
Qy 121 GlnThrLeuGluPheLeuLysIleProSerThrLeuAlaProProMetAspProSerVal 140
Db 384 CAAACTCTGGAATTTTAAAAATCCCTTCCACACTTGCACCCCATGGACCATCTGTG 443
Qy 141 ProIleTrpIleIlePheGlyValIlePheCysIleIleIleValAlaIleAlaLeu 160

Db 444 CCCATCTGGATTATTATATTGGTGTGATFATTTTGCATCATCATAGTTGCAATTGCACTA 503
Qy 161 LeuIleLeuSerGlyIleTrpGlnArgArgLysAsnLysGluProSerGluValAsp 180
Db 504 CTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTCTGAAGTGAT 563
Qy 181 AspAlaGluAspLysCysGluAsnMetIleThrIleGluAsnGlyIleProSerAspPro 200
Db 564 GACGCTGAAGATAAGTGTGAAGAACATGATCACAATTGAAAATGGCATCCCTCTGATCCC 623
Qy 201 LeuAspMetLysGly-GlyIleLeuMetMetProSer 212
Db 624 CTGGACATGAAGGGAGGGCATATTAAATGATGCCTTCA 660

RESULT 7
AX083392
LOCUS AX083392 1347 bp DNA linear PAT 28-FEB-2001
DEFINITION Sequence 84 from Patent WO0112660.
ACCESSION AX083392
VERSION AX083392.1 GI:13185232
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
AUTHORS Kato,S. and Kimura,T.
TITLE Human proteins having hydrophobic domains and dnas encoding these
JOURNAL Patent: WO 0112660-A 84 22-FEB-2001;
SAGAMI CHEMICAL RESEARCH CENTER (JP) ; Protegene Inc. (JP)

FEATURES
source Location/Qualifiers
1. .1347
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/db_xref="taxon:9606"
26. .694
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/codon_start=1
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/translation="MEMLLPFLVTAIHAELCQGAENAFKVRLSIRTAIGDKAYAWDT
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ORIGIN
Alignment Scores:
Pred. No.: 8.15e-113 Length: 1347
Score: 1089.00 Matches: 212
Percent Similarity: 99.53% Conservative: 0
Best Local Similarity: 99.53% Mismatches: 0
Query Match: 98.82% Indels: 1
DB: 6 Gaps: 0

US-09-989-724-387 (1-212) x AX083392 (1-1347)

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Db 26 ATGTTGTGGCTGCTCTTTTCTGGTGACTGCCATTGCTGAACCTCTGTCAACAGGT 85
Qy 21 AlaGluAsnAlaPheLysValArgLeuSerIleArgThrAlaLeuGlyAspLysAlaTyr 40
Db 86 GCAGAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAGCATAT 145
Qy 41 AlaTrpAspThrAsnGluGluTyrLeuPheLysAlaMetValAlaPheSerMetArgLys 60
Db 146 GCCTGGGATACCAATGAAGAAATACCTCTTCAAGCGATGGTAGCTTCTCCATGAGAAA 205
Qy 61 ValProAsnArgGluAlaThrGluIleSerHisValLeuLeuLeuValThrGlnArg 80

Db 206 GTTCCCAACAGAGAGCAAGCAAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGG 265

Qy 81 ValSerPheTrpPheValThrAspProSerLysAsnHisThrLeuProAlaValGlu 100

Db 266 GTATCAATCTGCTTGTGTGTACAGACCTTCAAAAATACACACCTTCTCTGCTGTTGAG 325

Qy 101 ValGlnSerAlaIleArgMetAsnLysAsnArgIleAsnAsnAlaPhePheLeuAsnAsp 120

Db 326 GTGCAATCAGCCCATAGAAATGAACAAGACCGGATCAACAATGCCCTTCTTTCTAAATGAC 385

Qy 121 GlnThrLeuGluPheLeuLysIleProSerThrLeuAlaProProMetAspProSerVal 140

Db 386 CAAACTCTGGAATTTTAAAAATCCCTTCCACACTTGACACCCCATGGACCCATCTGTG 445

Qy 141 ProIleTrpIleIlePheGlyValIlePheCysIleIleIleValAlaIleAlaLeu 160

Db 446 CCCATCTGGATTATTATTTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCCACTA 505

Qy 161 LeuIleLeuSerGlyIleTrpGlnArgArgLysAsnLysGluProSerGluValAsp 180

Db 506 CTGATTTTATCAGGGATCTGGCAACGTAGAAGAAACAAGAACCACTCTGAAGTGGAT 565

Qy 181 AspAlaGluAspLysCysGluAsnMetIleThrIleGluAsnGlyIleProSerAspPro 200

Db 566 GACGCTGAAGATAAGTGTGAACAATGATCACAATTTGAAATGGCATCCCTCTGATCCC 625

Qy 201 LeuAspMetLysGly-GlyIleLeuMetMetProSer 212

Db 626 CTGGACATGAAGGGAGGCGCATATTAAATGATGCCTTCA 662

RESULT 8

BC050606

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

2238257

12477932

2 (bases 1 to 1377)

Strausberg,R.

Direct Submission

Submitted (08-APR-2003) National Institutes of Health, Mammalian

Gene Collection (MGC), Cancer Genomics Office, National Cancer

Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,

BC050606 1377 bp mRNA linear PRI 12-NOV-2003

Homo sapiens kidney-specific membrane protein, mRNA (CDNA clone

MGC:60059 IMAGE:5183554), complete cds.

BC050606

BC050606.1 GI:30047080

MGC.

Homo sapiens (human)

Homo sapiens

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1377)

Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,

Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,

Altschul,S.P., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,

Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,

Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,

Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,

Scheetz,T.B., Brownstein,M.J., Ustin,T.B., Toshiyuki,S.,

Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,

Abramson,R.D., Mullany,S.J., Bosak,S.A., McEwan,P.J.,

McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,

Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,

Villalón,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,

Fahey,J., Helton,E., Kettman,M., Madan,A., Rodriguez,S.,

Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,

Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,

Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,

Butterfield,Y.S., Krzywinski,M.I., Skaleka,U., Smailus,D.E.,

Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.

Generation and initial analysis of more than 15,000 full-length

human and mouse cDNA sequences

Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

2238257

12477932

2 (bases 1 to 1377)

Strausberg,R.

Direct Submission

Submitted (08-APR-2003) National Institutes of Health, Mammalian

Gene Collection (MGC), Cancer Genomics Office, National Cancer

Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,

USA

NIH-MGC Project URL: <http://mgc.nci.nih.gov>

Contact: MGC help desk

Email: cgapbs-remail.nih.gov

Tissue Procurement: Life Technologies, Inc.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Sequencing Group at the Stanford Human Genome

Center, Stanford University School of Medicine, Stanford, CA 94305

Web site: <http://www-sbgc.stanford.edu>

Contact: (Dickson, Mark) mcd@paxil.stanford.edu

Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,

R. M.

Clone distribution: MGC clone distribution information can be found

through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>

Series: IRAK Plate: 110 Row: c Column: 4

This clone was selected for full length sequencing because it

passed the following selection criteria: matched mRNA gi: 21361864.

Location/Qualifiers

1..1377

/organism="Homo sapiens"

/mol_type="mRNA"

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/clone="MGC:60059 IMAGE:5183554"

/tissue_type="Colon, Kidney, Stomach, adult, whole pooled"

/clone_lib="NIH MGC_116"

/lab_host="DH10B"

/note="Vector: pCMV-SPORT6"

1..1377

/gene="NX17"

/note="synonym: NX-17"

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/db_xref="GI:30047081"

/db_xref="LocusID:57393"

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LTPL"

ORIGIN

Alignment Scores:

Pred. No.: 8.37e-113 Length: 1377

Score: 1089.00 Matches: 212

Percent Similarity: 99.53% Conservative: 0

Best Local Similarity: 99.53% Mismatches: 0

Query Match: 98.82% Indels: 1

DB: 9 Gaps: 0

US-09-989-724-387 (1-212) x BC050606 (1-1377)

Qy 1 MetLeuTrpLeuPhePheLeuValThrAlaIleHisAlaGluLeuCysGlnProGly 20

Db 9 ATGTTGGGCTGCTCTTTTCTGTTGACTGCCATTCATGCTGAACCTCTGTCACACGAGT 68

Qy 21 AlaGluAsnAlaPheLysValArgLeuSerIleArgThrAlaLeuGlyAspLysAlaTyr 40

Db 69 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGACAGCTCTGGGAGATAAGCATAT 128

Qy 41 AlaTrpAspThrAsnGluGluTyrLeuPheLysAlaMetValAlaPheSerMetArgLys 60

Db 129 GCCTGGGATACCAATGAAGAATACCTCTTCAAGCGATGGTAGCTTTCTCCATGAGAAA 188

Qy 61 ValProAsnArgGluAlaThrGluIleSerHisValLeuLeuCysAsnValThrGlnArg 80

Db 189 GTTCCCAACAGAGAGCAAGCAAGAAATTTCCCATGCTCTTGTGCAATGTAAACCCAGAG 248

Qy 81 ValSerPheTrpPheValThrAspProSerLysAsnHisThrLeuProAlaValGlu 100

Db 249 GTATCATTTCTGGTTGTGGTTACAGACCTTCAAAAAATCACACCTTCTCTGCTGTGAG 308
Qy 101 ValGlnSerAlaIleArgMetAsnLysAsnArgIleAsnAsnAlaPhePheLeuAsnAsp 120
Db 309 GTGCAATCAGCCATAAGAAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGAC 368
Qy 121 GlnThrLeuGluPheLeuLysIleProSerThrLeuAlaProProMetAspProSerVal 140
Db 369 CAAACTCTGGAAATTTTAAAAATCCCTTCCACACTTGACACCAACCATGACCATCTGTG 428
Qy 141 ProfileTrpIleIleIlePheGlyValIlePheCysIleIleIleValAlaIleAlaLeu 160
Db 429 CCCATCTGGATTATTATTGGTGTGATATTTCATCATCATAGTTGCAATGCACTA 488
Qy 161 LeuIleLeuSerGlyIleTrpGlnArgArgArgLysAsnLysGluProSerGluValAsp 180
Db 489 CTGATTTTATCAGGATCTGGCAACGTAGAGAAAGAACAAAGAACCATCTGAAGTGGAT 548
Qy 181 AspAlaGluAspLysCysGluAsnMetIleThrIleGluAsnGlyIleProSerAspPro 200
Db 549 GACGCTGAAGATAAGTGTGAAACATGATCACAATGAAATGGCATCCCTCTGATCCC 608
Qy 201 LeuAspMetLysGly-GlyIleLeuMetMetProSer 212
Db 609 CTGACATGAAGGAGGCGCATATTAAATGATGCCTTCA 645

RESULT 9
BC015099
LOCUS BC015099 1440 bp mRNA linear PRI 04-OCT-2003
DEFINITION Homo sapiens kidney-specific membrane protein, mRNA (cDNA clone
MGC:22827 IMAGE:3829035), complete cds.
ACCESSION BC015099
VERSION BC015099.1 GI:15929328
KEYWORDS MGC.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1440)
Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
Sheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,
McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
Fahey,J., Helton,E., Kettelman,M., Madan,A., Rodriguez,S.,
Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,
Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E.,
Schnurch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
22388257
12477932
2 (bases 1 to 1440)
Strausberg,R.
Direct Submission
Submitted (01-OCT-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
NIH-MGC Project URL: <http://mgc.nci.nih.gov>
Contact: MGC help desk
Email: cgaps-remail.nih.gov

Tissue Procurement: ATCC
cDNA Library Preparation: CLONTECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Institute for Systems Biology
<http://www.systemsbio.org>
contact: amadan@systemsbiology.org
Anup Madan, Jessica Fahey, Erin Helton, Mark Kettelman, Anuradha
Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting
Clone distribution: MGC clone distribution information can be found
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FEATURES
source

gene

CDS

ORIGIN

Alignment Scores:
Pred. No.: 8,84e-113 Length: 1440
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Query Match: 98.82% Indels: 1
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ACCESSION
BC014317 GI:15680012
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MGC.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 1605)
Strausberg,R.L., Feingold,B.A., Grouse,L.H., Derge,J.G.,
Klausner,R.D., Collins,P.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.P., Bhat,N.K.,
Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,
McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
Villalón,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
Fahey,J., Helton,E., Kettman,M., Madan,A., Young,A.C., Rodrigues,S.,
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Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E.,
Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
22388257
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12477932
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2 (bases 1 to 1605)
Strausberg,R.
AUTHORS
Direct Submission
TITLE
Submitted (17-SEP-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
NIH-MGC Project URL: <http://mgc.nci.nih.gov>
Contact: MGC help desk
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Institute for Systems Biology
<http://www.systemsbiology.org>
contact: amadan@systemsbiology.org
Anup Madan, Jessica Fahey, Erin Helton, Mark Kettelman, Anuradha

Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting
Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
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Percent Similarity: 99.53% Conservative: 0
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DEFINITION Sequence 27 from patent US 6312922.
ACCESSION AR177334
VERSION AR177334.1 GI:17919689
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 848)
AUTHORS Edwards,J.-B.Dumas,Milne., Duclert,A. and Bougueleret,L.
TITLE Complementary DNAs

JOURNAL Patent: US 6312922-A 27 06-NOV-2001;
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LOCUS BD247957 848 bp DNA linear PAT 17-JUL-2003
DEFINITION 5' ESTs for secreted proteins expressed in various tissues.
ACCESSION BD247957
VERSION BD247957.1 GI:33057727
KEYWORDS JP 2002525024-A/22.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

AUTHORS Edwards,J.B.D.M., Duclert,A. and Lacroix,B.
TITLE 5' ESTs for secreted proteins expressed in various tissues
JOURNAL Patent: JP 2002525024-A 22 13-AUG-2002;
GENSET
COMMENT OS Homo sapiens (human)
PN JP 2002525024-A/22
PD 13-AUG-2002
PF 31-JUL-1998 JP 2000505294
PR 01-AUG-1997 US 08/905051
PI JEAN BAPTISTE DUMAS MILNE EDWARDS,AYMERIC DUCLERT,BRUNO PI
LACROIX
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ORIGIN
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Best Local Similarity: 97.65% Mismatches: 4
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DEFINITION Sequence 27 from patent US 6573068.
ACCESSION AR340701
VERSION AR340701.1 GI:33732443
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 848)
AUTHORS Milne Edwards,J.-B.D., Duclert,A. and Bougueleret,L.
TITLE Claudin-50 protein
JOURNAL Patent: US 6573068-A 27 03-JUN-2003;
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Best Local Similarity: 97.65% Mismatches: 4
Query Match: 96.55% Indels: 1
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392 CAAACTCTGGAATTTTAAAAATCCCTTCCACACTTGCACCCACCCATGCCATCTGTG 451
Qy 141 ProIleTrpIleIlePheGlyValIlePheCysIleIleValAlaIleAlaLeu 160
Db |||||||
452 CCCATCTGGATTATTATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTA 511
Qy 161 LeuIleLeuSerGlyIleTrpGlnArgArgLysAsnLysGluProSerGluValAsp 180
Db |||||||
512 CTGATTTTATCAGGGATCTGGCAACCTADAAARAAGAACCAAGAACCATCTGAAGTGGAT 571
Qy 181 AspAlaGluAspLysCysGluAsnMetIleThrIleGluAsnGlyIleProSerAspPro 200
Db |||||||

Search completed: April 4, 2004, 03:09:42
Job time : 3777 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: April 3, 2004, 23:29:14 ; Search time 460 Seconds
(without alignments)
1957.865 Million cell updates/sec

Title: US-09-989-724-387

Perfect score: 1102

Sequence: 1 MLWLLPFLVTAIHAEACQPG.....ENGIPSDPLDMKGGILMMP 212

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delopt 6.0 , Delext 7.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DEV=xlh
-O=/cgn2 1/USPTO spool/US09989724/runat 31032004 081140 13280/app query.fasta_1.391
-DB=N Geneseq_29Jan04 -QFMT=fastap -SUFFIX=ring -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09989724 @CGN 1 1 470 @runat 31032004 081140 13280 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DLEXT=7

Database : N Geneseq_29Jan04:*

1: geneseqn1980s: *
2: geneseqn1990s: *
3: geneseqn2000s: *
4: geneseqn2001as: *
5: geneseqn2001bs: *
6: geneseqn2002as: *
7: geneseqn2003as: *
8: geneseqn2003bs: *
9: geneseqn2003cs: *
10: geneseqn2004s: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1102	100.0	1346	3	Aaz65097 Membrane-
2	1102	100.0	1346	3	Aac58612 Human PRO
3	1102	100.0	1346	3	Aaa77680 Human PRO
4	1102	100.0	1346	4	Aas21484 Human CDN
5	1102	100.0	1346	5	Aaf44243 Human PRO
6	1102	100.0	1346	7	Abx77959 Human PRO
7	1102	100.0	1346	7	Abx80371 Novel hum
8	1102	100.0	1346	7	ACA69277 Human CDN

9	1102	100.0	1346	7	ACD24093	Novel hum
10	1102	100.0	1346	7	ABX90348	Human sec
11	1102	100.0	1346	7	ABX64194	CDNA enco
12	1102	100.0	1346	7	ACA67234	CDNA enco
13	1102	100.0	1346	7	ACA64416	Novel hum
14	1102	100.0	1346	7	ACA03843	CDNA enco
15	1102	100.0	1346	7	ABX89381	DNA enco
16	1102	100.0	1346	7	ABX80875	Human sec
17	1102	100.0	1346	7	ACD44384	CDNA enco
18	1102	100.0	1346	7	ACD42035	Human sec
19	1102	100.0	1346	7	ABX79555	Human sec
20	1102	100.0	1346	7	ACA93576	Novel hum
21	1102	100.0	1346	7	ABX81258	Novel hum
22	1102	100.0	1346	7	ACA04264	Human CDN
23	1102	100.0	1346	7	ACA93074	Novel hum
24	1102	100.0	1346	7	ABX17158	Human PRO
25	1102	100.0	1346	8	ACA68013	Novel hum
26	1102	100.0	1346	8	ACA88462	Human sec
27	1102	100.0	1346	8	ACD81969	CDNA enco
28	1102	100.0	1346	8	ADA46000	Novel hum
29	1102	100.0	1346	8	ADA76431	Human PRO
30	1102	100.0	1346	8	ADA19081	Human PRO
31	1102	100.0	1346	8	ADA61704	Homo sapi
32	1102	100.0	1346	8	ADB19489	Novel hum
33	1102	100.0	1346	8	ADB28030	CDNA enco
34	1102	100.0	1346	8	ADA86509	Novel hum
35	1102	100.0	1346	8	ADB16073	Human PRO
36	1102	100.0	1346	8	ADA37897	Human CDN
37	1102	100.0	1346	8	ADA47859	Human PRO
38	1102	100.0	1346	8	ADA21583	Human CDN
39	1102	100.0	1346	8	ADA10370	Human CDN
40	1102	100.0	1346	8	ADA67654	Human PRO
41	1102	100.0	1346	8	ADB30661	CDNA enco
42	1102	100.0	1346	8	ADA85957	Novel hum
43	1102	100.0	1346	8	ADA17914	CDNA enco
44	1102	100.0	1346	8	ADA97169	Human PRO
45	1102	100.0	1346	8	ADA79473	Human PRO

ALIGNMENTS

RESULT 1

AAZ65097

ID AAZ65097 standard; cDNA; 1346 BP.

XX

AC AAZ65097;

XX

DT 05-APR-2000 (first entry)

XX

DE Membrane-bound protein PRO1312 encoding cDNA.

XX

KW Membrane-bound polypeptide; PRO polypeptide; LDL receptor; TIE ligand; pharmaceutical; receptor immunoadhesin; gene mapping; ss.

XX

OS Homo sapiens.

XX

PN WO9963088-A2.

XX

PD 09-DEC-1999.

XX

PF 02-JUN-1999; 99WO-US012252.

XX

PR 02-JUN-1998; 98US-0087607P.

PR 02-JUN-1998; 98US-0087609P.

PR 02-JUN-1998; 98US-0087759P.

PR 03-JUN-1998; 98US-0087827P.

PR 04-JUN-1998; 98US-0088021P.

PR 04-JUN-1998; 98US-0088025P.

PR 04-JUN-1998; 98US-0088028P.

PR 04-JUN-1998; 98US-0088029P.

PR 04-JUN-1998; 98US-0088030P.

PR 04-JUN-1998; 98US-0088033P.

PR 04-JUN-1998; 98US-0088326P.

PR 05-JUN-1998; 98US-0088167P.
PR 05-JUN-1998; 98US-0088202P.
PR 05-JUN-1998; 98US-0088212P.
PR 05-JUN-1998; 98US-0088217P.
PR 09-JUN-1998; 98US-0088655P.
PR 10-JUN-1998; 98US-0088722P.
PR 10-JUN-1998; 98US-0088730P.
PR 10-JUN-1998; 98US-0088734P.
PR 10-JUN-1998; 98US-0088738P.
PR 10-JUN-1998; 98US-0088740P.
PR 10-JUN-1998; 98US-0088741P.
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PR 11-JUN-1998; 98US-0088858P.
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PR 16-JUN-1998; 98US-0089440P.
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PR 16-JUN-1998; 98US-0089514P.
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PR 17-JUN-1998; 98US-0089598P.
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PR 17-JUN-1998; 98US-0089600P.
PR 17-JUN-1998; 98US-0089653P.
PR 18-JUN-1998; 98US-0089801P.
PR 18-JUN-1998; 98US-0089907P.
PR 19-JUN-1998; 98US-0089947P.
PR 19-JUN-1998; 98US-0089948P.
PR 19-JUN-1998; 98US-0089952P.
PR 22-JUN-1998; 98US-0090246P.
PR 22-JUN-1998; 98US-0090252P.
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PR 23-JUN-1998; 98US-0090349P.
PR 23-JUN-1998; 98US-0090355P.
PR 24-JUN-1998; 98US-0090429P.
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PR 24-JUN-1998; 98US-0090445P.
PR 24-JUN-1998; 98US-0090461P.
PR 24-JUN-1998; 98US-0090472P.
PR 24-JUN-1998; 98US-0090535P.
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PR 24-JUN-1998; 98US-0090540P.
PR 24-JUN-1998; 98US-0090557P.
PR 25-JUN-1998; 98US-0090676P.
PR 25-JUN-1998; 98US-0090688P.
PR 25-JUN-1998; 98US-0090690P.
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PR 25-JUN-1998; 98US-0090694P.
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PR 25-JUN-1998; 98US-0090696P.
PR 26-JUN-1998; 98US-0090862P.
PR 26-JUN-1998; 98US-0090863P.
PR 01-JUL-1998; 98US-0091358P.
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PR 02-JUL-1998; 98US-0091478P.
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PR 02-JUL-1998; 98US-0091519P.
PR 02-JUL-1998; 98US-0091544P.
PR 02-JUL-1998; 98US-0091626P.
PR 02-JUL-1998; 98US-0091628P.
PR 02-JUL-1998; 98US-0091633P.

PR 02-JUL-1998; 98US-0091646P.
PR 02-JUL-1998; 98US-0091673P.
PR 07-JUL-1998; 98US-0091978P.
PR 07-JUL-1998; 98US-0091982P.
PR 09-JUL-1998; 98US-0092182P.
PR 10-JUL-1998; 98US-0092472P.
PR 20-JUL-1998; 98US-0093339P.
PR 30-JUL-1998; 98US-0094651P.
PR 04-AUG-1998; 98US-0095282P.
PR 04-AUG-1998; 98US-0095285P.
PR 04-AUG-1998; 98US-0095301P.
PR 04-AUG-1998; 98US-0095302P.
PR 04-AUG-1998; 98US-0095318P.
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PR 10-AUG-1998; 98US-0095916P.
PR 10-AUG-1998; 98US-0095929P.
PR 10-AUG-1998; 98US-0096012P.
PR 11-AUG-1998; 98US-0096143P.
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PR 12-AUG-1998; 98US-0096329P.
PR 17-AUG-1998; 98US-0096757P.
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PR 17-AUG-1998; 98US-0096768P.
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PR 17-AUG-1998; 98US-0096894P.
PR 17-AUG-1998; 98US-0096895P.
PR 17-AUG-1998; 98US-0096897P.
PR 18-AUG-1998; 98US-0096949P.
PR 18-AUG-1998; 98US-0096950P.
PR 18-AUG-1998; 98US-0096959P.
PR 18-AUG-1998; 98US-0096960P.
PR 18-AUG-1998; 98US-0097022P.
PR 19-AUG-1998; 98US-0097141P.
PR 20-AUG-1998; 98US-0097218P.
PR 24-AUG-1998; 98US-0097661P.
PR 26-AUG-1998; 98US-0097951P.
PR 26-AUG-1998; 98US-0097952P.
PR 26-AUG-1998; 98US-0097954P.
PR 26-AUG-1998; 98US-0097955P.
PR 26-AUG-1998; 98US-0097971P.
PR 26-AUG-1998; 98US-0097974P.
PR 26-AUG-1998; 98US-0097978P.
PR 26-AUG-1998; 98US-0097979P.
PR 26-AUG-1998; 98US-0097986P.
PR 26-AUG-1998; 98US-0098014P.
PR 31-AUG-1998; 98US-0098525P.
PR 16-SEP-1998; 98US-0100634P.
PR 12-JAN-1999; 99US-0115565P.

(GETH) GENENTECH INC.

Baker K, Chen J, Goddard A, Gurney AL, Smith V, Watanabe CK;
Wood WI, Yuan J;

WPI; 2000-072883/06.
P-PSDB; AAY66751.

Membrane-bound proteins and related nucleotide sequences.

Claim 2; Fig 277; 822pp; English.

The invention provides membrane-bound PRO polypeptides and polynucleotides encoding them. The PRO sequences of the invention were identified based on extracellular domain homology screening. The PRO sequences have homology with proteins including LDL receptors, TIG ligands and various enzymes. The membrane-bound proteins and receptor molecules are useful as pharmaceutical and diagnostic agents. Receptor immunoadhesins, for instance, can be used as therapeutic agents to block receptor-ligand interactions. The membrane-bound proteins can also be

CC employed for screening of potential peptide or small molecule inhibitors
CC of the relevant receptor/ligand interaction. The PRO encoding sequences
CC are useful as hybridization probes, in chromosome and gene mapping and in
CC the generation of antisense RNA and DNA. PRO nucleic acid sequences will
CC also be useful for the preparation of PRO polypeptides, especially by
CC recombinant techniques
XX
SQ Sequence 1346 BP; 457 A; 245 C; 237 G; 407 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 1.26e-123 Length: 1346
Score: 1102.00 Matches: 212
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0

US-09-989-724-387 (1-212) x AA265097 (1-1346)

QY 1 MetLeuTrpLeuLeuPhePheLeuValThrAlaIleHisAlaGluLeuCysGlnProGly 20
DB 7 ATGTTGGTGGTCTCTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACAGGT 66
QY 21 AlaGluAsnAlaPheLysValArgLeuSerIleArgThrAlaLeuGlyAspLysAlaTyr 40
DB 67 GCAGAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAGCATAT 126
QY 41 AlaTrpAspThrAsnGluGluTyrLeuPheLysAlaMetValAlaPheSerMetArgLys 60
DB 127 GCCTGGGATACCAATGAAGAATACTCTTCAAGCGATGGTAGCTTTCTCCATGAGAAA 186
QY 61 ValProAsnArgGluAlaThrGluIleSerHisValLeuLeuCysAsnValThrGlnArg 80
DB 187 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGCTCTACTTTGCAATGTAAACAGAG 246
QY 81 ValSerPheTrpPheValValThrAspProSerLysAsnHisThrLeuProAlaValGlu 100
DB 247 GTATCATCTCTGGTTGTGTTACAGACCTTCAAAAATCAACACCTTCTCTGCTGTGAG 306
QY 101 ValGlnSerAlaIleArgMetAsnLysAsnArgIleAsnAsnAlaPhePheLeuAsnAsp 120
DB 307 GTGCAATCAGCCATAAGAATGAACAAGACCGGATCAACAATGCTTCTTCTAAATGAC 366
QY 121 GlnThrLeuGluPheLeuLysIleProSerThrLeuAlaProMetAspProSerVal 140
DB 367 CAACCTCTGGAATTTTAAATATCCCTTCCCACTTGCAACCCATGGACCATCTGTG 426
QY 141 ProIleTrpIleIlePheGlyValIlePheCysIleIleIleValAlaIleAlaLeu 160
DB 427 CCCATCTGGATTATATATTGGTGTGATATTGTCATCATCATGATGCAATGCACTA 486
QY 161 LeuIleLeuSerGlyIleTrpGlnArgArgArgLysAsnLysGluProSerGluValAsp 180
DB 487 CTGATTTTATCAGGGATCTGGCAACGTAGAGAAGAAGAACCAAGAACCATCTGAAGTGGAT 546
QY 181 AspAlaGluAspLysCysGluAsnMetIleThrIleGluAsnGlyIleProSerAspPro 200
DB 547 GACGCTGAAGATAAGTGTGAACAATGATCAAAATGAAATGGCATCCCTCTGATCCC 606
QY 201 LeuAspMetLysGlyGlyIleLeuMetMetProSer 212
DB 607 CTGGACATGAAGGGGGCATATTAATGATGCTTCA 642

RESULT 2

AAC58612
ID AAC58612 standard; cDNA; 1346 BP.

XX AAC58612;

AC AAC58612;

XX 29-JAN-2001 (first entry)

DT Human PRO1312 protein UNQ678 encoding cDNA SEQ ID NO:160.

XX

KW Human; immune related disease; diagnosis; antiinflammatory; cardiac;
KW dermatological; antiarthritic; antirheumatic; immunosuppressive;
KW haemostatic; antithyroid; antidiabetic; nootropic; neuroprotective;
KW antianaemic; hepatotropic; virucide; antipsoriatic; antiallergic;
KW antiasthmatic; systemic lupus erythematosus; rheumatoid arthritis;
KW osteoarthritis; spondyloarthropathy; systemic sclerosis; sarcoidosis;
KW idiopathic inflammatory myopathy; Sjogren's syndrome; thyroiditis;
KW systemic vasculitis; autoimmune haemolytic anaemia; diabetes mellitus;
KW autoimmune thrombocytopaenia; immune-mediated renal disease;
KW demyelinating disease; hepatobiliary disease; Whipple's disease;
KW inflammatory bowel disease; gluten-sensitive enteropathy;
KW autoimmune disease; immune-mediated skin disease; allergic disease;
KW immunological disease; transplantation associated disease;
KW graft rejection; graft-versus-host-disease; ss.
OS Homo sapiens.
XX
XX WO200053758-A2.
PN 14-SEP-2000.
XX
PD 02-MAR-2000; 2000WO-US005841.
XX
PR 08-MAR-1999; 99WO-US005028.
PR 10-MAR-1999; 99US-0123618P.
PR 12-MAR-1999; 99US-0123957P.
PR 23-MAR-1999; 99US-0125775P.
PR 12-APR-1999; 99US-0128849P.
PR 20-APR-1999; 99WO-US008615.
PR 28-APR-1999; 99US-0131445P.
PR 04-MAY-1999; 99US-0132371P.
PR 14-MAY-1999; 99US-0134287P.
PR 02-JUN-1999; 99WO-US012252.
PR 23-JUN-1999; 99US-0141037P.
PR 20-JUL-1999; 99US-0144758P.
PR 26-JUL-1999; 99US-0145698P.
PR 28-JUL-1999; 99US-0146222P.
PR 01-SEP-1999; 99WO-US020111.
PR 08-SEP-1999; 99WO-US020594.
PR 13-SEP-1999; 99WO-US020944.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 05-OCT-1999; 99WO-US023089.
PR 29-OCT-1999; 99US-0162506P.
PR 29-NOV-1999; 99WO-US028214.
PR 30-NOV-1999; 99WO-US028313.
PR 30-NOV-1999; 99WO-US028409.
PR 01-DEC-1999; 99WO-US028301.
PR 01-DEC-1999; 99WO-US028634.
PR 02-DEC-1999; 99WO-US028551.
PR 02-DEC-1999; 99WO-US028564.
PR 02-DEC-1999; 99WO-US028565.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030999.
PR 30-DEC-1999; 99WO-US031274.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000277.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 18-FEB-2000; 2000WO-US004342.
PR 22-FEB-2000; 2000WO-US004414.
XX
PA (GETH) GENENTECH INC.
XX
PI Ashkenazi AJ, Baker KP, Goddard A, Gurney AL, Hebert C, Henzel W;
PI Kabakoff RC, Lu Y, Pan J, Pennica D, Shelton DL, Smith V;
PI Stewart TA, Tumas D, Watanabe CK, Wood WI, Yan M;
XX WPI; 2000-572271/53.
DR P-PSDB; AAB33447.
XX
PT Sixty four PRO polypeptides, useful in the diagnosis and treatment of

PT immune related disorders, e.g. systemic lupus erythematosus, rheumatoid
PT arthritis, osteoarthritis, thyroiditis and diabetes mellitus.

PS Claim 23; Fig 67; 309pp; English.

XX
CC The present invention describes sixty four human PRO proteins which can
CC be used in the treatment of immune related diseases. The human PRO
CC proteins, anti-PRO antibodies, agonists and antagonists are useful for
CC treating and diagnosing immune related disorders. The disorders are
CC selected from systemic lupus erythematosus, rheumatoid arthritis,
CC osteoarthritis, juvenile chronic arthritis, spondyloarthropathies,
CC systemic sclerosis, idiopathic inflammatory myopathies, Sjogren's
CC syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic
CC anaemia, autoimmune thrombocytopenia, thyroiditis, diabetes mellitus,
CC immune-mediated renal disease, demyelinating diseases of the central and
CC peripheral nervous systems, hepatobiliary diseases, inflammatory bowel
CC disease, gluten-sensitive enteropathy and Whipple's disease, autoimmune
CC or immune-mediated skin diseases, allergic diseases, immunological
CC diseases of the lung, and transplantation associated diseases including
CC graft rejection and graft-versus-host-disease. AAC58397 to AAC58578
CC represent PCR primers and hybridisation probes used in the isolation of
CC human PRO sequences. AAC58579 to AAC58642 and AAB33414 to AAB33477
CC represent human PRO polynucleotide and protein sequences given in the
CC exemplification of the present invention

SQ Sequence 1346 BP; 457 A; 245 C; 237 G; 407 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 1.26e-123 Length: 1346
Score: 1102.00 Matches: 212
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0

US-09-989-724-387 (1-212) x AAC58612 (1-1346)

Qy 1 MetLeuTrpLeuLeuPhePheLeuValThrAlaIleHisAlaGluLeuCysGlnProGly 20
Db 7 ATGTTGGTGGTCTCTTTTCTGGTACTGCCATTTCATGCTGAACTGTGCAACCCAGGT 66
Qy 21 AlaGluAsnAlaPheLysValArgLeuSerIleArgThrAlaLeuGlyAspLysAlaTyr 40
Db 67 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 126
Qy 41 AlaTrpAspThrAsnGluGluTyrLeuPheLysAlaMetValAlaPheSerMetArgLys 60
Db 127 GCCTGGGATACCAATGAAGAATACCTCTCAAGCGATGGTAGCTTTCTCCATGAGAAA 186
Qy 61 ValProAsnArgGluAlaThrGluIleSerHisValLeuLeuLeuCysAsnValThrGlnArg 80
Db 187 GTTCCCAACAGAGAGAACAGAAATTTCCCATGCTTCTACTTTTGCAATGTAAACCCAGAG 246
Qy 81 ValSerPheTrpPheValValThrAspProSerLysAsnHisThrLeuProAlaValGlu 100
Db 247 GTATCATTTCTGGTTTGTGTTACAGACCCCTTCAAAAATCAACACCCCTTCTGCTGTGAG 306
Qy 101 ValGlnSerAlaIleArgMetAsnLysAsnArgIleAsnAsnAlaPhePheLeuAsnAsp 120
Db 307 GTGCAATCAGCCCATAGAATGAACAGAACCGGATCAACAATGCCCTTCTTTCTAAATGAC 366
Qy 121 GlnThrLeuGluPheLeuLysIleProSerThrLeuAlaProProMetAspProSerVal 140
Db 367 CAAACTCTGGAATTTTAAAAATCCCTTCCACACTTGCACCCACCCATGACCCCATCTGTG 426
Qy 141 ProIleTrpIleIlePheGlyValIlePheCysIleIleIleValAlaIleAlaLeu 160
Db 427 CCCATCTGGATTATTATTTGGTGTGATTTTGTGATCATCATCATAGTTGCAATGCACTA 486
Qy 161 LeuIleLeuSerGlyIleTrpGlnArgArgLysAsnLysGluProSerGluValAsp 180
Db 487 CTGATTTTATCAGGGATCTGGCAACGTTAGAAGAAAGAAAGAAAGAACCATCTGAAGTGGAT 546

Qy 181 AspAlaGluAspLysCysGluAsnMetIleThrIleGluAsnGlyIleProSerAspPro 200
Db 547 GACGCTGAAGATAAGTGTGAAACACATGATCACAAATTGAAATGGCATCCCTCTGATCCC 606
Qy 201 LeuAspMetLysGlyGlyIleLeuMetMetProSer 212
Db 607 CTGGACATGAAGGGGGGCATATTAAATGATGCTTCA 642
RESULT 3
AAA77680
ID AAA77680 standard; cDNA; 1346 BP.
XX
AC AAA77680;
XX
DT 07-NOV-2000 (first entry)
XX
DE Human PRO1312 cDNA sequence SEQ ID NO:213.
XX
KW Human; PRO; promotion; inhibition; angiogenesis; cardiovascularisation;
KW diagnosis; trauma; wound; cancer; atherosclerosis; cardiac hypertrophy;
KW angiogenic; proliferative; cardiac; cardiovascular; antiatherosclerotic;
KW cytostatic; gene therapy; vaccine; ss.
XX
OS Homo sapiens.
XX
PN WO200032221-A2.
XX
PD 08-JUN-2000.
XX
PF 30-NOV-1999; 99WO-US028313.
XX
PR 01-DEC-1998; 98WO-US025108.
PR 16-DEC-1998; 98US-0112850P.
PR 12-JAN-1999; 99US-0115554P.
PR 08-MAR-1999; 99WO-US005028.
PR 12-MAR-1999; 99US-0123957P.
PR 28-APR-1999; 99US-0131445P.
PR 14-MAY-1999; 99US-0134287P.
PR 02-JUN-1999; 99WO-US012252.
PR 23-JUN-1999; 99US-0141037P.
PR 20-JUL-1999; 99US-0144758P.
PR 26-JUL-1999; 99US-0145698P.
PR 01-SEP-1999; 99WO-US020111.
PR 08-SEP-1999; 99WO-US020594.
PR 13-SEP-1999; 99WO-US020944.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 05-OCT-1999; 99WO-US023089.
PR 29-OCT-1999; 99US-0162506P.
XX
PA (GETH) GENENTECH INC.
XX
PI Ashkenazi AJ, Baker KP, Ferrara N, Gerber H, Hillan KJ;
PI Goddard A, Godowski PJ, Gurney AL, Klein RD, Kuo SS, Paoni NF;
PI Smith V, Watanabe CK, Williams PM, Wood WI;
XX
DR WPI; 2000-412154/35.
DR P-PSDB; AAB24430.
XX
PT Nucleic acids encoding PRO polypeptides useful for preventing, diagnosing
PT and treating diagnosing a cardiovascular, endothelial or angiogenic
PT disorders in mammals.
XX
PS Claim 61; Fig 85; 315pp; English.
XX
CC The present invention describes nucleic acids encoding PRO polypeptides
CC useful for preventing, diagnosing and treating disorder in mammals by
CC cardiovascular, endothelial or angiogenic disorder in mammals by
CC modulating cell proliferation, angiogenesis and cardiovascularisation,
CC and for identifying agonists and antagonists of these processes. The
CC nucleic acids and the proteins they encode may be used in the prevention,
CC treatment and diagnosis of diseases associated with inappropriate PRO
CC expression such as cardiovascular, endothelial or angiogenic disorders in

CC mammals (e.g. atherosclerosis, cancers and cardiac hypertrophy). For
CC example, the nucleic acids (NCs) and vectors containing them and the PRO
CC polypeptide may be used to treat disorders associated with decreased PRO
CC expression. AAA77510 to AAA77721 and AAB24388 to AAB24435 represent
CC nucleotide and protein sequences used in the exemplification of the
CC present invention
XX

SQ Sequence 1346 BP; 457 A; 245 C; 237 G; 407 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 1.26e-123 Length: 1346
Score: 1102.00 Matches: 212
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0

US-09-989-724-387 (1-212) x AAA77680 (1-1346)

QY 1 MetLeuTrpLeuLeuPhePheLeuValThrAlaIleHisAlaGluLeuCysGlnProGly 20
DB 7 ATGTGTGGCTGCTCTTTTCTGTGACTGCCATTCATGCTGAACCTGTCAACAGGT 66
QY 21 AlaGluAsnAlaPheLysValArgLeuSerIleArgThrAlaLeuGlyAspLysAlaTyr 40
DB 67 GCAGAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAGCATAT 126
QY 41 AlaTrpAspThrAsnGluGluTyrLeuPheLysAlaMetValAlaPheSerMetArgLys 60
DB 127 GCCTGGGATACCAATGAAGATACCTCTTCAAGCGATGGTAGTTTCTCCATGAGAAA 186
QY 61 ValProAsnArgGluAlaThrGluIleSerHisValLeuLeuCysAsnValThrGlnArg 80
DB 187 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCTTGTCAATGTAAACCCAGG 246
QY 81 ValSerPheTrpPheValValThrAspProSerLysAsnHisThrLeuProAlaValGlu 100
DB 247 GTATCATCTCTGTTTGTGTTACAGACCTTCAAAAATCACACCTTCTCTGTTGAG 306
QY 101 ValGlnSerAlaIleArgMetAsnLysAsnArgIleAsnAsnAlaPhePheLeuAsnAsp 120
DB 307 GTGCAATCAGCCATAAGATGAACAGAACCGGATCAACATGCCTTCTTTCAATGAC 366
QY 121 GlnThrLeuGluPheLeuLysIleProSerThrLeuAlaProMetAspProSerVal 140
DB 367 CAAACTCTGGAAATTTTAAATCCCTTCCACACTTGCACCCATGGACCCATCTGTG 426
QY 141 ProIleTrpIleIlePheGlyValIlePheCysIleIleIleValAlaIleAlaLeu 160
DB 427 CCCATCTGGATTATTATTTGGTGTGATATTTGTCATCATATAGTTGCAATTGCACTA 486
QY 161 LeuIleLeuSerGlyIleTrpGlnArgArgLysAsnLysGluProSerGluValAsp 180
DB 487 CTGATTTTATCAGGGATCTGGCAACGTAGAGAAAGAACAAAGAACCATCTGAAGTGGAT 546
QY 181 AspAlaGluAspLysCysGluAsnMetIleThrIleGluAsnGlyIleProSerAspPro 200
DB 547 GACGCTGAAGATAAGTGTGAACAATGATCATCAATTTGAAATGGCATCCCTCTGATCCC 606
QY 201 LeuAspMetLysGlyIleLeuMetMetProSer 212
DB 607 CTGGACATGAAGGGGGGCATATTATGATGCCTTCA 642

RESULT 4

AAS21484

ID AAS21484 standard; cDNA; 1346 BP.

XX

AC AAS21484;

XX

DT 24-OCT-2001 (first entry)

XX

DE Human cDNA sequence encoding for PRO1312 polypeptide.

XX

KW Human secretory and transmembrane; PRO; mammalian; cancer; lung; breast;
KW prostate; cervical; tumour necrosis factor-alpha; TNF-alpha; cartilage;
KW ear; proliferation; glucose; free fatty acid; skeletal muscle; adipocyte;
KW A-peptide; factor VIIA; gene therapy; ss.
XX
OS Homo sapiens.
XX
PN WO200140466-A2.
XX
PD 07-JUN-2001.
XX
XX 01-DEC-2000; 2000WO-US032678.
PF
XX
PR 01-DEC-1999; 99WO-US028301.
PR 01-DEC-1999; 99WO-US028634.
PR 02-DEC-1999; 99WO-US028551.
PR 02-DEC-1999; 99WO-US028564.
PR 02-DEC-1999; 99WO-US028565.
PR 09-DEC-1999; 99US-0170262P.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 20-DEC-1999; 99WO-US030999.
PR 30-DEC-1999; 99WO-US031243.
PR 30-DEC-1999; 99WO-US031274.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000277.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 18-FEB-2000; 2000WO-US004342.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US004914.
PR 24-FEB-2000; 2000WO-US005004.
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005841.
PR 03-MAR-2000; 2000US-0187202P.
PR 10-MAR-2000; 2000WO-US006319.
PR 15-MAR-2000; 2000WO-US006884.
PR 20-MAR-2000; 2000WO-US007377.
PR 21-MAR-2000; 2000WO-US007532.
PR 30-MAR-2000; 2000WO-US008439.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 05-JUN-2000; 2000US-0209832P.
PR 28-JUL-2000; 2000WO-US020710.
PR 11-AUG-2000; 2000WO-US022031.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000WO-US030952.
PR 10-NOV-2000; 2000WO-US030873.
XX
XX (GETH) GENENTECH INC.
XX
PI Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;
PI Gerritsen MB, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
XX
DR WPI; 2001-408281/43.
DR P-PSDB; AAU12412.
XX
PT Isolated, secretory and transmembrane PRO polypeptide used to detect
PT other PRO polypeptides, link bioactive molecules to cells expressing PRO
PT polypeptides, and detect the presence of mammalian tumors e.g. lung,
PT breast, prostate, cervical.
XX
PS Claim 3; Fig 481; 813pp; English.
XX
CC AAS21244-AAS21518 encode for novel human secretory and transmembrane PRO
CC polypeptides. The PRO polypeptides are useful to detect other PRO
CC polypeptides, to link bioactive molecules to cells expressing PRO
CC polypeptides, to modulate biological activities of cells expressing PRO

CC polypeptides, and to detect the presence of mammalian lung, colon,
CC breast, prostate, rectal, cervical or liver tumours by comparing PRO
CC polypeptide expression in a cell sample to that in a control sample. Some
CC of the 275 sequences are also useful to stimulate the release of tumour
CC necrosis factor-alpha (TNF-alpha) from human blood, the proliferation or
CC differentiation of chondrocytes, the proliferation or gene expression in
CC pericyte cells, the release of proteoglycans from cartilage, the
CC proliferation of inner ear utricular supporting cells or of T-
CC lymphocytes, the release of a cytokine from peripheral blood monocytes
CC (PBMCs), or the proliferation of endothelial cells. Some of the PRO
CC polypeptides may modulate glucose or free fatty acid uptake by skeletal
CC muscle cells or by adipocytes; or inhibit binding of A-peptide to factor
CC VIIA. The PRO polypeptides can be used in assays to identify molecules
CC involved in binding interactions. The polynucleotides encoding PRO
CC polypeptides can be used to generate probes, antisense RNA/DNA,
CC transgenic or knock out animals and can be used in gene therapy
XX
SQ Sequence 1346 BP; 457 A; 245 C; 237 G; 407 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 1.26e-123 Length: 1346
Score: 1102.00 Matches: 212
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-09-989-724-387 (1-212) x AAS21484 (1-1346)

Qy 1 MetLeuTrpLeuLeuPheLeuValThrAlaIleHisAlaGluLeuCysGlnProGly 20
Db 7 ATGTTGGTGCTCTCTTTTCTGGTGAGTGCCTATTCAGTCTGTCAACCCAGGT 66
Qy 21 AlaGluAsnAlaPheLeuValArgLeuSerIleArgThrAlaLeuGlyAspLysAlaTyr 40
Db 67 GCAGAAATGCTTTTAAAGTGAGACTTACTATCAGAACAGCTCTGGAGATAAAGCATAT 126
Qy 41 AlaTrpAspThrAsnGluGluTyrLeuPheLysAlaMetValAlaPheSerMetArgLys 60
Db 127 GCCTGGGATACCAATGAAGAATACCTTCAAAGCGATGTAGCTTTCTCCATGAGAAA 186
Qy 61 ValProAsnArgGluAlaThrGluIleSerHisValLeuLeuCysAsnValThrGlnArg 80
Db 187 GTTCCCAACAGAGAGCAACAGAAATTTCCCATGTCTTACTTGTCAATTAACCCAGAGG 246
Qy 81 ValSerPheTrpPheValValThrAspProSerLysAsnHisThrLeuProAlaValGlu 100
Db 247 GTATCAATCTGGTTTGTGGTTACAGACCTTCAAATAATCACACCTTCTCTGTGTGAG 306
Qy 101 ValGlnSerAlaIleArgMetAsnLysAsnArgIleAsnAsnAlaPhePheLeuAsnAsp 120
Db 307 GTGCAATCAGCCATAGATGAACAGAACCGGATCAACATGCCCTTCTTCTAAATGAC 366
Qy 121 GlnThrLeuGluPheLeuLysIleProSerThrLeuAlaProProMetAspProSerVal 140
Db 367 CAAACTCTGGAAATTTTAAATAATCCCTTCCACACTTGCACACCCATGGACCCATCTGTG 426
Qy 141 ProIleTrpIleIleIlePheGlyValIlePheCysIleIleIleValAlaIleAlaLeu 160
Db 427 CCCATCTGGATTATTATATTGGTGATATTTTGCATCATCATAGTTGCAATTGCACTA 486
Qy 161 LeuIleLeuSerGlyIleTrpGlnArgArgLysAsnLysGluProSerGluValAsp 180
Db 487 CTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAAGTGAT 546
Qy 181 AspAlaGluAspLysCysGluAsnMetIleThrIleGluAsnGlyIleProSerAspPro 200
Db 547 GACGCTGAAGATAAGTGTGAACACATGATCACAATTGAATGAAATGGCATCCCTCTGATCCC 606
Qy 201 LeuAspMetLysGlyGlyIleLeuMetMetProSer 212
Db 607 CTGGACATGAAGGGGGGCATATTATATGATGCTTCA 642

RESULT 5

AAF44243

ID AAF44243 standard; cDNA; 1346 BP.

XX AAF44243;

AC AAF44243;

XX 02-APR-2001 (first entry)

XX Human PRO1312 (UNQ678) nucleotide sequence SEQ ID NO:386.

XX Human; secreted and transmembrane protein; PRO; cytostatic; cell death;

XX cancer; chromosomal mapping; gene mapping; tissue typing;

XX diagnostic assay; ss.

XX Homo sapiens.

XX WO200073454-A1.

XX 07-DEC-2000.

XX 30-MAR-2000; 2000WO-US008439.

XX 02-JUN-1999; 99WO-US012252.

XX 23-JUN-1999; 99US-0141037P.

XX 07-JUL-1999; 99US-0143048P.

XX 20-JUL-1999; 99US-0144758P.

XX 26-JUL-1999; 99US-0145698P.

XX 28-JUL-1999; 99US-0146222P.

XX 17-AUG-1999; 99US-0149396P.

XX 15-SEP-1999; 99WO-US021090.

XX 15-SEP-1999; 99WO-US021547.

XX 08-OCT-1999; 99US-0158663P.

XX 30-NOV-1999; 99WO-US028313.

XX 01-DEC-1999; 99WO-US028301.

XX 16-DEC-1999; 99WO-US030095.

XX 20-DEC-1999; 99WO-US030911.

XX 05-JAN-2000; 2000WO-US000219.

XX 06-JAN-2000; 2000WO-US000376.

XX 11-FEB-2000; 2000WO-US003565.

XX 18-FEB-2000; 2000WO-US004341.

XX 22-FEB-2000; 2000WO-US004414.

XX 24-FEB-2000; 2000WO-US005004.

XX 02-MAR-2000; 2000WO-US005841.

XX 15-MAR-2000; 2000WO-US006884.

XX 20-MAR-2000; 2000WO-US007377.

XX (GETH) GENENTECH INC.

XX Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;

XX Ferrara N, Fong S, Gerber H, Gerritsen MB, Goddard A, Godowski PJ;

XX Grimaldi CJ, Gurney AL, Kljavin IJ, Napier MA, Pan J, Paoni NF;

XX Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;

XX Zhang Z;

XX WPI; 2001-032160/04.

XX P-PSDB; AAB65274.

XX PRO polynucleotides used to produce polypeptides used to target bioactive
XX molecules such as toxins, radiolabels or antibodies, to specific cells,
XX to cause targeted cell death.

XX Claim 2; Fig 277; 935pp; English.
XX The present invention describes human secreted and transmembrane PRO
XX proteins. The PRO proteins have cytostatic activity. The PRO proteins can
XX be used for targeted delivery of bioactive molecules, such as toxins,
XX radiolabels or antibodies, that cause cell death. PRO nucleotide
XX sequences, and their fragments, can be used as hybridisation probes, in
XX chromosomal and gene mapping, and in the generation of anti-sense RNA and
XX DNA. They may also be used to produce transgenic animals which are used
XX to develop and screen therapeutically useful reagents. The PRO nucleotide
XX and protein sequence can be used for tissue typing and in treating

CC cancer. Anti-PRO antibodies can be used in diagnostic assays. AAF44270 to
CC AAF44470 represent PCR primers and hybridisation probes used in the
CC isolation of human PRO sequences. AAF44087 to AAF44269 and AAB65154 to
CC AAB65300 represent human PRO polynucleotide and protein sequences given
CC in the exemplification of the present invention
XX
SQ Sequence 1346 BP; 457 A; 245 C; 237 G; 407 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 1.26e-123 Length: 1346
Score: 1102.00 Matches: 212
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 5 Gaps: 0

US-09-989-724-387 (1-212) x AAF44243 (1-1346)

Qy 1 MetLeuTrpLeuLeuPhePheLeuValThrAlaIleHisAlaGluLeuCysGlnProGly 20
Db 7 ATGTTGGTGGCTCTTTTCTGGTACGACCTAGTATCAGAACAGCTCTGGAGATAAGCATAT 66
Qy 21 AlaGluAsnAlaPheLysValArgLeuSerIleArgThrAlaLeuGlyAspLysAlaTyr 40
Db 67 GCAGAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGAGATAAGCATAT 126
Qy 41 AlaTrpAspThrAsnGluGluTyrLeuPheLysAlaMetValAlaPheSerMetArgLys 60
Db 127 GCCTGGGATACCAATGAAGATACCTCTTCAAGCGATGGTAGCTTCTCCATGAGAAA 186
Qy 61 ValProAsnArgGluAlaThrGluIleSerHisValLeuLeuCysAsnValThrGlnArg 80
Db 187 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCTTCTTGAATGTAAATGAC 246
Qy 81 ValSerPheTrpPheValValThrAspProSerLysAsnHisThrLeuProAlaValGlu 100
Db 247 GTATCATCTCTGTTTGTGGTTACAGACCTTCAAAAATCACACCTTCTCTGCTGTGAG 306
Qy 101 ValGlnSerAlaIleArgMetAsnLysAsnArgIleAsnAsnAlaPhePheLeuAsnAsp 120
Db 307 GTGCAATCAGCCATAAGATGAACAGACCGGATCAACATGCCTTCTTTCTAAATGAC 366
Qy 121 GlnThrLeuGluPheLeuLysIleProSerThrLeuAlaProMetAspProSerVal 140
Db 367 CAAACTCTGGAAATTTTAAATCCCTTCCCACTTGCACCCATGGACCCATCTGTG 426
Qy 141 ProIleTrpIleIleIlePheGlyValIlePheCysIleIleIleValAlaIleAlaLeu 160
Db 427 CCCATCTGGATTATTATTTGGTGTGATTTTGCATCATCATAGTTGCATTCACATA 486
Qy 161 LeuIleLeuSerGlyIleTrpGlnArgArgArgLysAsnLysGluProSerGluValAsp 180
Db 487 CTGATTTTATCAGGATCTGGCAACGTAGAGAAGAACCAAGAACCATCTGAAGTGGAT 546
Qy 181 AspAlaGluAspLysCysGluAsnMetIleThrIleGluAsnGlyIleProSerAspPro 200
Db 547 GACGCTGAAGATAAGTGTGAACACATGATCACAATTTGAATGGCATCCCTCTGATCCC 606
Qy 201 LeuAspMetLysGlyIleLeuMetMetProSer 212
Db 607 CTGGACATGAAGGGGGCATATTAAATGATGCCTTCA 642

RESULT 6

ABX77959

ID ABX77959 standard; cDNA; 1346 BP.

XX

AC ABX77959;

XX 14-APR-2003 (first entry)

XX Human PRO polynucleotide #121.

DE Human; PRO; gene; ss; cytostatic; tumour; cancer; breast; lung; stomach;

XX

KW

KW liver; horse; cow; dog; cat; sheep; pig; goat; rabbit; ADEPT;
KW antibody-dependent enzyme mediated prodrug therapy.
XX Homo sapiens.
OS
XX US2003027163-A1.
PN
XX
PD 06-FEB-2003.
XX
PF 15-NOV-2001; 2001US-00997666.
XX
PR 16-JUN-1997; 97US-0049787P.
PR 17-OCT-1997; 97US-0062250P.
PR 05-NOV-1997; 97WO-US020069.
PR 12-NOV-1997; 97US-0065186P.
PR 13-NOV-1997; 97US-0065311P.
PR 24-NOV-1997; 97US-0066770P.
PR 25-FEB-1998; 98US-0075945P.
PR 20-MAR-1998; 98US-0078910P.
PR 28-APR-1998; 98US-0083322P.
PR 07-MAY-1998; 98US-0084600P.
PR 28-MAY-1998; 98US-0087106P.
PR 02-JUN-1998; 98US-0087607P.
PR 02-JUN-1998; 98US-0087609P.
PR 02-JUN-1998; 98US-0087759P.
PR 03-JUN-1998; 98US-0087827P.
PR 04-JUN-1998; 98US-0088021P.
PR 04-JUN-1998; 98US-0088025P.
PR 04-JUN-1998; 98US-0088026P.
PR 04-JUN-1998; 98US-0088028P.
PR 04-JUN-1998; 98US-0088029P.
PR 04-JUN-1998; 98US-0088030P.
PR 04-JUN-1998; 98US-0088033P.
PR 04-JUN-1998; 98US-0088326P.
PR 05-JUN-1998; 98US-0088167P.
PR 05-JUN-1998; 98US-0088202P.
PR 05-JUN-1998; 98US-0088212P.
PR 05-JUN-1998; 98US-0088217P.
PR 09-JUN-1998; 98US-0088655P.
PR 10-JUN-1998; 98US-0088734P.
PR 10-JUN-1998; 98US-0088738P.
PR 10-JUN-1998; 98US-0088742P.
PR 10-JUN-1998; 98US-0088810P.
PR 10-JUN-1998; 98US-0088824P.
PR 10-JUN-1998; 98US-0088826P.
PR 11-JUN-1998; 98US-0088858P.
PR 11-JUN-1998; 98US-0088861P.
PR 11-JUN-1998; 98US-0088876P.
PR 12-JUN-1998; 98US-0089105P.
PR 16-JUN-1998; 98US-0089440P.
PR 16-JUN-1998; 98US-0089512P.
PR 16-JUN-1998; 98US-0089514P.
PR 17-JUN-1998; 98US-0089532P.
PR 17-JUN-1998; 98US-0089538P.
PR 17-JUN-1998; 98US-0089598P.
PR 17-JUN-1998; 98US-0089599P.
PR 17-JUN-1998; 98US-0089600P.
PR 17-JUN-1998; 98US-0089653P.
PR 18-JUN-1998; 98US-0089801P.
PR 18-JUN-1998; 98US-0089907P.
PR 18-JUN-1998; 98US-0089908P.
PR 19-JUN-1998; 98US-0089947P.
PR 19-JUN-1998; 98US-0089948P.
PR 19-JUN-1998; 98US-0089952P.
PR 22-JUN-1998; 98US-0090246P.
PR 22-JUN-1998; 98US-0090252P.
PR 22-JUN-1998; 98US-0090254P.
PR 23-JUN-1998; 98US-0090349P.
PR 23-JUN-1998; 98US-0090355P.
PR 24-JUN-1998; 98US-0090429P.
PR 24-JUN-1998; 98US-0090431P.
PR 24-JUN-1998; 98US-0090435P.
PR 24-JUN-1998; 98US-0090444P.

PR 24-JUN-1998; 98US-0090445P.
PR 24-JUN-1998; 98US-0090472P.
PR 24-JUN-1998; 98US-0090535P.
PR 24-JUN-1998; 98US-0090540P.
PR 24-JUN-1998; 98US-0090542P.
PR 24-JUN-1998; 98US-0090557P.
PR 25-JUN-1998; 98US-0090676P.
PR 25-JUN-1998; 98US-0090678P.
PR 25-JUN-1998; 98US-0090690P.
PR 25-JUN-1998; 98US-0090694P.
PR 25-JUN-1998; 98US-0090695P.
PR 25-JUN-1998; 98US-0090696P.
PR 25-JUN-1998; 98US-0090862P.
PR 26-JUN-1998; 98US-0090863P.
PR 01-JUL-1998; 98US-0091360P.
PR 01-JUL-1998; 98US-0091544P.
PR 02-JUL-1998; 98US-0091478P.
PR 02-JUL-1998; 98US-0091519P.
PR 02-JUL-1998; 98US-0091626P.
PR 02-JUL-1998; 98US-0091628P.
PR 02-JUL-1998; 98US-0091633P.
PR 02-JUL-1998; 98US-0091646P.
PR 02-JUL-1998; 98US-0091673P.
PR 07-JUL-1998; 98US-0091978P.
PR 07-JUL-1998; 98US-0091982P.
PR 09-JUL-1998; 98US-0092182P.
PR 10-JUL-1998; 98US-0092472P.
PR 20-JUL-1998; 98US-0093339P.
PR 30-JUL-1998; 98US-0094651P.
PR 04-AUG-1998; 98US-0095282P.
PR 04-AUG-1998; 98US-0095285P.
PR 04-AUG-1998; 98US-0095301P.
PR 04-AUG-1998; 98US-0095302P.
PR 04-AUG-1998; 98US-0095318P.
PR 04-AUG-1998; 98US-0095321P.
PR 04-AUG-1998; 98US-0095325P.
PR 10-AUG-1998; 98US-0095916P.
PR 10-AUG-1998; 98US-0095929P.
PR 10-AUG-1998; 98US-0096012P.
PR 11-AUG-1998; 98US-0096143P.
PR 11-AUG-1998; 98US-0096146P.
PR 12-AUG-1998; 98US-0096329P.
PR 17-AUG-1998; 98US-0096757P.
PR 17-AUG-1998; 98US-0096766P.
PR 17-AUG-1998; 98US-0096768P.
PR 17-AUG-1998; 98US-0096773P.
PR 17-AUG-1998; 98US-0096791P.
PR 17-AUG-1998; 98US-0096867P.
PR 17-AUG-1998; 98US-0096891P.
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PR 20-AUG-1998; 98US-0097218P.
PR 24-AUG-1998; 98US-0097661P.
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PR 31-AUG-1998; 98US-0098525P.
PR 16-SEP-1998; 98US-0100634P.
PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98US-0100858P.

PR 17-SEP-1998; 98WO-US019437.
PR 07-OCT-1998; 98WO-US021141.
PR 01-DEC-1998; 98WO-US025108.
PR 22-DEC-1998; 98US-0113296P.
PR 05-JAN-1999; 99WO-US000106.
PR 08-MAR-1999; 99WO-US005028.
PR 12-MAR-1999; 99US-0123957P.
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PR 23-JUN-1999; 99US-0141037P.
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PR 28-JUL-1999; 99US-0146222P.
PR 17-AUG-1999; 99US-0149396P.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 08-OCT-1999; 99US-0158663P.
PR 30-NOV-1999; 99WO-US028313.
PR 01-DEC-1999; 99WO-US028301.
PR 01-DEC-1999; 99WO-US028634.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US004914.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 10-MAR-2000; 2000WO-US006319.
PR 15-MAR-2000; 2000WO-US006884.
PR 20-MAR-2000; 2000WO-US007377.
PR 30-MAR-2000; 2000WO-US008439.
PR 15-MAY-2000; 2000WO-US013358.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 23-JUN-2000; 2000US-0213637P.
PR 28-JUL-2000; 2000WO-US020710.
PR 11-AUG-2000; 2000WO-US022031.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 07-SEP-2000; 2000US-0230978P.

Alignment Scores:

Pred. No.: 1.26e-123 Length: 1346
Score: 1102.00 Matches: 212
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 7 Gaps: 0

US-09-989-724-387 (1-212) x ABX77959 (1-1346)

QY 1 MetLeuTrpLeuLeuPhePheLeuValThrAlaIleHisAlaGluLeuCysGlnProGly 20
Db 7 ATGTTGTGGCTGCTCTTTTCTGTGACTGCCATTCAATGCTGAACCTCTGTCAACCAGGT 66
QY 21 AlaGluAsnAlaPheLysValArgLeuSerIleArgThrAlaLeuGlyAspLysAlaTyr 40
Db 67 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 126
QY 41 AlaTrpAspThrAsnGluGluTyrLeuPheLysAlaMetValAlaPheSerMetArgLys 60
Db 127 GCCTGGGATACCAATGAAGAATACCTCTTCAAGCGATGGTAGCTTTCTCCATGAGAAA 186
QY 61 ValProAsnArgGluAlaThrGluIleSerHisValLeuLeuCysAsnValThrGlnArg 80
Db 187 GTTCCCAACAGAGACAGCAACAGAAATTCCTCATGTCTTACTTTTGCAATGTAAACCCAGAG 246
QY 81 ValSerPheTrpPheValValThrAspProSerLysAsnHisThrLeuProAlaValGlu 100

Db 247 GTATCATCTGGTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCTGCTGTGAG 306
Qy 101 ValGlnSerAlaIleArgMetAsnLysAsnArgIleAsnAsnAlaPhePheLeuAsnAsp 120
Db 307 GTGCAATCAGCCATAAGAATGAACAAGACCGATCAACAATGCCCTTCTTCTAATGAC 366
Qy 121 GlnThrLeuGluPheLeuLysIleProSerThrLeuAlaProProMetAspProSerVal 140
Db 367 CAAACTCTGGAATTTTAAAAATCCCTTCCACACTTGCACCCACCCATGGACCCATCTGTG 426
Qy 141 ProIleTIpIleIleIlePheGlyValIlePheCysIleIleIleValAlaIleAlaLeu 160
Db 427 CCCATCTGGATTATTATATTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTA 486
Qy 161 LeuIleLeuSerGlyIleTIpGlnArgArgArgLysAsnLysGluProSerGluValAsp 180
Db 487 CTGATTTTATCAGGGATCTGGCAACCTAGAGAAGAAACAAGAACCATCTGAAGTGGAT 546
Qy 181 AspAlaGluAspLysCysGluAsnMetIleThrIleGluAsnGlyIleProSerAspPro 200
Db 547 GACGCTGAAGATAAGTGTGAACAACATGATCACAATTGAAATGGCATCCCTCTGTATCCC 606
Qy 201 LeuAspMetLysGlyGlyIleLeuMetMetProSer 212
Db 607 CTGGACATGAAGGGGGGCATATTATATGATGCTTCA 642

RESULT 7

ID ABX80371 standard; DNA; 1346 BP.
XX
AC ABX80371;
XX
DT 28-APR-2003 (first entry)
XX
DE Novel human secreted or transmembrane protein PRO1192 DNA.
XX
KW Human; PRO; hypertrophy of neonatal heart; angiogenesis; wound healing;
KW cardiac insufficiency disorder; cancer; tumour; immune response;
KW adrenal cortical capillary endothelial growth; c-fos induction;
KW vascular endothelial growth factor inhibition; VEGF inhibition;
KW endothelial cell growth inhibitor; T-lymphocytes stimulation;
KW retinal neurons cell survival; rod photoreceptor cell survival;
KW retinal disorder; retinitis pigmentosa; kidney disorder;
KW mammalian kidney mesangial cell proliferation; Berger disease;
KW dermatitis; herpeticiformis; Crohn's disease; chondrocyte proliferation;
KW chondrocyte redifferentiation; sports injury; arthritis; gene; ds.
XX
OS Homo sapiens.
XX
PN US2002132252-A1.
XX
PD 19-SEP-2002.
XX
PF 14-NOV-2001; 2001US-00990442.
XX
PR 16-JUN-1997; 97US-0049787P.
PR 17-OCT-1997; 97US-0062250P.
PR 05-NOV-1997; 97WO-US020069.
PR 12-NOV-1997; 97US-0065186P.
PR 13-NOV-1997; 97US-0065311P.
PR 24-NOV-1997; 97US-0066770P.
PR 25-FEB-1998; 98US-0075945P.
PR 20-MAR-1998; 98US-0078910P.
PR 28-APR-1998; 98US-0083322P.
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PR 04-JUN-1998; 98US-0088025P.

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PR 16-JUN-1998; 98US-0089440P.
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PR 16-JUN-1998; 98US-0089514P.
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PR 18-JUN-1998; 98US-0089801P.
PR 18-JUN-1998; 98US-0089907P.
PR 18-JUN-1998; 98US-0089908P.
PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98WO-US019437.
PR 07-OCT-1998; 98WO-US021141.
PR 01-DEC-1998; 98WO-US025108.
PR 05-JAN-1999; 99WO-US000106.
PR 08-MAR-1999; 99WO-US005028.
PR 02-JUN-1999; 99WO-US012252.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 30-NOV-1999; 99WO-US028313.
PR 01-DEC-1999; 99WO-US028301.
PR 01-DEC-1999; 99WO-US028634.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 06-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US004914.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 10-MAR-2000; 2000WO-US006319.
PR 15-MAR-2000; 2000WO-US006884.
PR 20-MAR-2000; 2000WO-US007377.
PR 30-MAR-2000; 2000WO-US008439.
PR 15-MAY-2000; 2000WO-US013358.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 11-AUG-2000; 2000WO-US022031.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000WO-US030952.
PR 01-DEC-2000; 2000WO-US032678.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-JUN-2001; 2001WO-US017800.
PR 20-JUN-2001; 2001WO-US019692.

29-JUN-2001; 2001WO-US021066.
09-JUL-2001; 2001WO-US021735.
28-AUG-2001; 2001US-00941992.
(GETH) GENENTECH INC.
Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ;
Grimaldi JC, Gurney AL, Kijavini IJ, Napier MA, Pan J, Paoni NF;
Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;
Zhang Z;
WPI; 2003-247083/24.
P-PSDB; ABUS9168.
Novel isolated PRO polypeptides e.g., PRO826, PRO1068, PRO1184, PRO1346
and PRO1375, which stimulate proliferation of stimulated T-lymphocytes
are therapeutically useful for enhancing immune response and in cancer
treatments.
Claim 2; Fig 279; 648pp; English.
The invention describes an isolated human PRO polypeptide. The PRO
polypeptides are useful in detecting PRO polypeptides in a sample, in
linking a bioactive molecule to a cell expressing a PRO polypeptide, and
in modulating at least one biological activity of a cell expressing a PRO
polypeptide. PRO1312 stimulates hypertrophy of neonatal heart and is thus
useful for treating cardiac insufficiency disorders. PRO1154 and PRO1186
stimulate adrenal cortical capillary endothelial growth, and PRO536,
PRO943, PRO828, PRO1068 or PRO535, PRO826, PRO819, PRO1126,
PRO1360 and PRO1387 induce c-fos in endothelial cells, and are thus
useful for treating conditions or disorders where angiogenesis would be
beneficial, e.g. wound healing and antagonist of this polypeptide are
useful for treating cancerous tumours. PRO812 inhibits vascular
endothelial growth factor (VEGF) stimulated endothelial cell growth in
cells and is thus useful for inhibiting endothelial cell growth in
mammals which would be beneficial in inhibiting tumour growth. PRO826,
PRO1068, PRO1184, PRO1346 and PRO1375 stimulate proliferation of
stimulated T-lymphocytes and are therapeutically useful for enhancing
immune response. PRO828, PRO826, PRO1068 or PRO1132 enhance survival of
retinal neurons cells (PRO1132 is also enhances survival/proliferation of
rod photoreceptor cells) and therefore are useful for treating retinal
disorders of injuries, e.g. retinitis pigmentosa, AMD. PRO819, PRO813
and PRO1066 induce proliferation of mammalian kidney mesangial cells,
and therefore are useful for treating kidney disorders associated with
decreased mesangial cell function such as Berger disease or other
nephropathies associated with dermatitis, herpeticiformis or Crohn's
disease. PRO1310, PRO844, PRO1312, PRO1192 and PRO1387 induce the
proliferation and/or redifferentiation of chondrocytes in culture and are
thus useful for treating sports injuries, and arthritis. This sequence
represents a novel human PRO protein polynucleotide
SQ Sequence 1346 BP; 457 A; 245 C; 237 G; 407 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 1.26e-123 Length: 1346
Score: 1102.00 Matches: 212
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 7 Gaps: 0

US-09-989-724-387 (1-212) x ABX80371 (1-1346)

Qy 1 MetLeuTrpLeuPheLeuValThrAlaIleHisAlaGluLeuCysGlnProGly 20
Db 7 ATGTTGGTGCTCTCTTTTCTGGTGAGTCCATTCTGCTGAACCTCTGTCAACCAAGT 66
Qy 21 AlaGluAanAlaPheLysValArgLeuSerIleArgThrAlaLeuGlyAspLysAlaTyr 40
Db 67 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAGCATAT 126
Qy 41 AlaTrpAspThrAsnGluGluTyrLeuPheLysAlaMetValAlaPheSerMetArgLys 60

Db 127 GCCTGGGATACCAATGAAGATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAA 186
Qy 61 ValProAsnArgGluAlaThrGluIleSerHisValLeuLeuCysAsnValThrGlnArg 80
Db 187 GTTCCCAACAGAGAGCAACAGAAATTTCCCATGTCTCTACTTGTCAATGTAAACCCAGAG 246
Qy 81 ValSerPheTrpPheValValThrAspProSerLysAsnHisThrLeuProAlaValGlu 100
Db 247 GTATCATCTGGTTTGGTTACAGACCCCTTCAAAAAATCACACCCCTTCTCTGCTGTGAG 306
Qy 101 ValGlnSerAlaIleArgMetAsnLysAsnArgIleAsnAsnAlaPhePheLeuAsnAsp 120
Db 307 GTGCAATCAGCCATAAGAAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAATGAC 366
Qy 121 GlnThrLeuGluPheLeuLysIleProSerThrLeuAlaProProMetAspProSerVal 140
Db 367 CAAACTCTGGAAATTTTAAAAATCCCTTCCACACTTGCACACCCATGGACCCATCTGTG 426
Qy 141 ProIleTrpIleIleIlePheGlyValIlePheCysIleIleIleValAlaIleAlaLeu 160
Db 427 CCCATCTGGATTATTATATTGGTGTGATATTTTGCATCATCATAGTTGCAATGCACTA 486
Qy 161 LeuIleLeuSerGlyIleTrpGlnArgArgArgLysAsnLysGluProSerGluValAsp 180
Db 487 CTGATTTTATCAGGGATCTGGCAACGTAGAGAAGAAAGAACCAACCATCTGAAGTGGAT 546
Qy 181 AspAlaGluAspLysCysGluAsnMetIleThrIleGluAsnGlyIleProSerAspPro 200
Db 547 GACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCTCTGATCCC 606
Qy 201 LeuAspMetLysGlyIleLeuMetMetProSer 212
Db 607 CTGGACATGAAGCGGGGGCATATTAAATGATGCCTTCA 642

RESULT 8
ACA69277
ID ACA69277 standard; cDNA; 1346 BP.
XX ACA69277;
AC ACA69277;
XX 26-JUN-2003 (first entry)
XX Human cDNA encoding secreted/transmembrane protein PRO1312.
DE Human; ss; gene; PRO; secreted protein; transmembrane protein;
KW cardiac insufficiency disorders; angiogenesis; wound healing;
KW cancerous tumour; immune response; retinal disorder; sight loss;
KW retinitis pigmentosa; age-related macular degeneration; AMD;
KW kidney disorder; Berger disease; nephropathy; dermatitis; herpeticiformis;
KW Crohn's disease; sports injury; arthritis.
XX Homo sapiens.
OS US2003032023-A1.
XX 13-FEB-2003.
XX 14-NOV-2001; 2001US-00990711.
XX 16-JUN-1997; 97US-0049787P.
XX 17-OCT-1997; 97US-0062250P.
XX 05-NOV-1997; 97WO-US020069.
XX 12-NOV-1997; 97US-0065186P.
XX 13-NOV-1997; 97US-0065311P.
XX 24-NOV-1997; 97US-0066770P.
XX 25-FEB-1998; 98US-0075945P.
XX 20-MAR-1998; 98US-0078910P.
XX 28-APR-1998; 98US-0083322P.
XX 07-MAY-1998; 98US-0084600P.
XX 28-MAY-1998; 98US-0087106P.
XX 02-JUN-1998; 98US-0087607P.
XX 02-JUN-1998; 98US-0087609P.

PR 02-JUN-1998; 98US-0087759P.
PR 03-JUN-1998; 98US-0087827P.
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PR 09-JUL-1998; 98US-0092182P.
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PR 18-AUG-1998; 98US-0097022P.
PR 19-AUG-1998; 98US-0097141P.
PR 20-AUG-1998; 98US-0097218P.
PR 24-AUG-1998; 98US-0097661P.
PR 26-AUG-1998; 98US-0097952P.
PR 26-AUG-1998; 98US-0097954P.
PR 26-AUG-1998; 98US-0097955P.
PR 26-AUG-1998; 98US-0097971P.
PR 26-AUG-1998; 98US-0097974P.
PR 26-AUG-1998; 98US-0097978P.
PR 26-AUG-1998; 98US-0097979P.
PR 26-AUG-1998; 98US-0097986P.
PR 26-AUG-1998; 98US-0098014P.
PR 31-AUG-1998; 98US-0098525P.
PR 16-SEP-1998; 98US-0100634P.
PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98US-0100858P.
PR 17-SEP-1998; 98WO-US019437.
PR 07-OCT-1998; 98WO-US021141.
PR 01-DEC-1998; 98WO-US025108.
PR 22-DEC-1998; 98US-0113296P.
PR 05-JAN-1999; 99WO-US000106.
PR 08-MAR-1999; 99WO-US005028.
PR 12-MAR-1999; 99US-0123957P.
PR 02-JUN-1999; 99WO-US012252.
PR 23-JUN-1999; 99US-0141037P.
PR 07-JUL-1999; 99US-0143048P.
PR 20-JUL-1999; 99US-0144758P.
PR 26-JUL-1999; 99US-0145698P.
PR 28-JUL-1999; 99US-0146222P.
PR 17-AUG-1999; 99US-0149396P.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 08-OCT-1999; 99US-0158663P.
PR 30-NOV-1999; 99WO-US028313.
PR 01-DEC-1999; 99WO-US028301.
PR 01-DEC-1999; 99WO-US028634.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000376.

PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US004914.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 10-MAR-2000; 2000WO-US006319.
PR 15-MAR-2000; 2000WO-US006884.
PR 20-MAR-2000; 2000WO-US007377.
PR 30-MAR-2000; 2000WO-US008439.
PR 15-MAY-2000; 2000WO-US013358.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 23-JUN-2000; 2000US-0213637P.
PR 28-JUL-2000; 2000WO-US020710.
PR 11-AUG-2000; 2000WO-US022031.

Alignment Scores:

Pred. No.: 1.26e-123 Length: 1346
Score: 1102.00 Matches: 212
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 7 Gaps: 0

US-09-989-724-387 (1-212) x ACA69277 (1-1346)

QY 1 MetLeuTrpLeuPhePheLeuValThrAlaIleHisAlaGluLeuCysGlnProGly 20
DB 7 ATGTTGGTCTGCTCTTTTCTGGTGACTGCCATTTCATGCTGAACCTGTCAACAGGT 66
QY 21 AlaGluAsnAlaPheLysValArgLeuSerIleArgThrAlaLeuGlyAspLysAlaTyr 40
DB 67 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 126
QY 41 AlaTrpAspThrAsnGluGluTyrLeuPheLysAlaMetValAlaPheSerMetArgLys 60
DB 127 GCCTGGGATACCAATGAAGAAATACCTCTTCAAGCGATGGTAGCTTTCTCCATGAGAAA 186
QY 61 ValProAsnArgGluAlaThrGluIleSerHisValLeuLeuCysAsnValThrGlnArg 80
DB 187 GTTCCCAACAGAGAGCAACAGAAATTTCCCATGCTCTTTCATGATGAACCCAGAGG 246
QY 81 ValSerPheTrpPheValThrAspProSerLysAsnHisThrLeuProAlaValGlu 100
DB 247 GTATCATCTGTTTGTGTTTACAGACCTTCAAAAAATCAACATGCCCTTCTGCTGTTGAG 306
QY 101 ValGlnSerAlaIleArgMetAsnLysAsnArgIleAsnAsnAlaPhePheLeuAsnAsp 120
DB 307 GTGCAATCAGCCATAGAATGAACAGAACCGGATCAACAATGCCCTTCTTCTTAATGAC 366
QY 121 GlnThrLeuGluPheLeuLysIleProSerThrLeuAlaProProMetAspProSerVal 140
DB 367 CAAACTCTGGAATTTTAAAAATCCCTTCCACACTTGACACCCACCCACCCATCTGTG 426
QY 141 ProIleTrpIleIleIlePheGlyValIlePheCysIleIleIleValAlaIleAlaLeu 160
DB 427 CCCATCTGGATTATTATATTGTTGTTGATATTTTGCATCATCATAGTTGCAATTGCAC 486
QY 161 LeuIleLeuSerGlyIleTrpGlnArgArgLysAsnLysGluProSerGluValAsp 180
DB 487 CTGATTTTATCAGGGATCTGGCAACGTTAGAGAAAGAACAAAGAACCATCTGAAGTGGAT 546
QY 181 AspAlaGluAspLysCysGluAsnMetIleThrIleGluAsnGlyIleProSerAspPro 200
DB 547 GACGCTGAAGATAAGTGTGAAGAACATGATCACAATTTGAAATGGCATCCCTCTGATCC 606
QY 201 LeuAspMetLysGlyIleLeuMetMetProSer 212
DB 607 CTGGACATGAAGGGGGGCATATTATATGATGCTTCA 642

RESULT 9
ACD24093
ID ACD24093 standard; cDNA; 1346 BP.
XX
AC ACD24093;
DT 26-AUG-2003 (first entry)
XX
DB Novel human secreted and transmembrane protein PRO1312 cDNA.
XX
KW Human; secreted and transmembrane protein; PRO; antiinflammatory;
KW antiarteriosclerotic; cardiant; anti-infertility; anti-HIV; cytostatic;
KW antidiabetic; gene therapy; tumour necrosis factor (TNF)-alpha release;
KW TNF-alpha release; cell proliferation; cell differentiation;
KW gene expression modulator; proteoglycan release; cytokine release;
KW tumour; inflammatory disease; organ failure; atherosclerosis;
KW cardiac injury; infertility; birth defect; premature aging; AIDS;
KW acquired immunodeficiency syndrome; cancer; diabetic complication;
KW chromosome mapping; gene mapping; pharmaceutical; diagnostic; biosensor;
KW bio reactor; tissue typing; gene; ss.
XX
OS Homo sapiens.
XX
PN US2003032156-A1.
XX
PD 13-FEB-2003.
XX
PF 06-MAY-2002; 2002US-00140474.
XX
PR 31-MAR-1997; 97WO-US005230.
PR 12-JUN-1998; 98WO-US012456.
PR 14-JUL-1998; 98WO-US014552.
PR 28-AUG-1998; 98WO-US017888.
PR 10-SEP-1998; 98WO-US018824.
PR 14-SEP-1998; 98WO-US019093.
PR 14-SEP-1998; 98WO-US019094.
PR 14-SEP-1998; 98WO-US019177.
PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98WO-US019437.
PR 07-OCT-1998; 98WO-US021141.
PR 29-OCT-1998; 98WO-US022991.
PR 29-OCT-1998; 98WO-US022992.
PR 20-NOV-1998; 98WO-US024855.
PR 01-DEC-1998; 98WO-US025108.
PR 05-JAN-1999; 99WO-US000106.
PR 08-MAR-1999; 99WO-US005028.
PR 10-MAR-1999; 99WO-US005190.
PR 20-APR-1999; 99WO-US008615.
PR 14-MAY-1999; 99WO-US010733.
PR 02-JUN-1999; 99WO-US012252.
PR 01-SEP-1999; 99WO-US020111.
PR 08-SEP-1999; 99WO-US020594.
PR 13-SEP-1999; 99WO-US020944.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 05-OCT-1999; 99WO-US023089.
PR 29-NOV-1999; 99WO-US028214.
PR 30-NOV-1999; 99WO-US028313.
PR 30-NOV-1999; 99WO-US028409.
PR 01-DEC-1999; 99WO-US028301.
PR 01-DEC-1999; 99WO-US028634.
PR 02-DEC-1999; 99WO-US028551.
PR 02-DEC-1999; 99WO-US028564.
PR 02-DEC-1999; 99WO-US028565.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 20-DEC-1999; 99WO-US030999.
PR 22-DEC-1999; 99WO-US030720.
PR 30-DEC-1999; 99WO-US031243.
PR 30-DEC-1999; 99WO-US031274.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000277.
PR 06-JAN-2000; 2000WO-US000376.

Qy 201 LeuAspMetLysGlyGlyLeuMetMetProSer 212
Db 607 CTGGACATGAAGGGGGCATATTATATGATGCTTCA 642

RESULT 10
ABX90348
ID ABX90348 standard; cDNA; 1346 BP.
XX ABX90348;
AC
XX
DT 01-MAY-2003 (first entry)
DE Human secreted/transmembrane protein cDNA, #157.
XX
KW Human; gene; ss; PRO; secreted; transmembrane; signal peptide;
KW pharmaceutical; diagnostic; therapeutic; gene therapy.
XX
OS Homo sapiens.
XX
PN US2002160384-A1.
XX
PD 31-OCT-2002.
XX
PF 14-NOV-2001; 2001US-00992598.
XX
PR 16-JUN-1997; 97US-0049787P.
PR 17-OCT-1997; 97US-0062250P.
PR 05-NOV-1997; 97WO-US020069.
PR 12-NOV-1997; 97US-0065186P.
PR 13-NOV-1997; 97US-0065311P.
PR 24-NOV-1997; 97US-0066770P.
PR 25-FEB-1998; 98US-0075945P.
PR 20-MAR-1998; 98US-0078910P.
PR 07-MAY-1998; 98US-0083322P.
PR 28-APR-1998; 98US-0084600P.
PR 07-MAY-1998; 98US-0087106P.
PR 28-MAY-1998; 98US-0087607P.
PR 02-JUN-1998; 98US-0087609P.
PR 02-JUN-1998; 98US-0087759P.
PR 03-JUN-1998; 98US-0087827P.
PR 04-JUN-1998; 98US-0088021P.
PR 04-JUN-1998; 98US-0088025P.
PR 04-JUN-1998; 98US-0088026P.
PR 04-JUN-1998; 98US-0088028P.
PR 04-JUN-1998; 98US-0088029P.
PR 04-JUN-1998; 98US-0088030P.
PR 04-JUN-1998; 98US-0088033P.
PR 04-JUN-1998; 98US-0088326P.
PR 05-JUN-1998; 98US-0088167P.
PR 05-JUN-1998; 98US-0088202P.
PR 05-JUN-1998; 98US-0088212P.
PR 05-JUN-1998; 98US-0088217P.
PR 09-JUN-1998; 98US-0088655P.
PR 10-JUN-1998; 98US-0088734P.
PR 10-JUN-1998; 98US-0088738P.
PR 10-JUN-1998; 98US-0088742P.
PR 10-JUN-1998; 98US-0088810P.
PR 10-JUN-1998; 98US-0088824P.
PR 10-JUN-1998; 98US-0088826P.
PR 11-JUN-1998; 98US-0088858P.
PR 11-JUN-1998; 98US-0088861P.
PR 11-JUN-1998; 98US-0088876P.
PR 12-JUN-1998; 98US-0089105P.
PR 16-JUN-1998; 98US-0089440P.
PR 16-JUN-1998; 98US-0089512P.
PR 16-JUN-1998; 98US-0089514P.
PR 17-JUN-1998; 98US-0089532P.
PR 17-JUN-1998; 98US-0089538P.
PR 17-JUN-1998; 98US-0089598P.
PR 17-JUN-1998; 98US-0089599P.
PR 17-JUN-1998; 98US-0089600P.
PR 17-JUN-1998; 98US-0089653P.

PR 18-JUN-1998; 98US-0089801P.
PR 18-JUN-1998; 98US-0089907P.
PR 18-JUN-1998; 98US-0089908P.
PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98WO-US019437.
PR 07-OCT-1998; 98WO-US021141.
PR 01-DEC-1998; 98WO-US025108.
PR 05-JAN-1999; 99WO-US000106.
PR 08-MAR-1999; 99WO-US005028.
PR 02-JUN-1999; 99WO-US012252.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 30-NOV-1999; 99WO-US028313.
PR 01-DEC-1999; 99WO-US028301.
PR 01-DEC-1999; 99WO-US028634.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US004914.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 10-MAR-2000; 2000WO-US006319.
PR 15-MAR-2000; 2000WO-US006884.
PR 20-MAR-2000; 2000WO-US007377.
PR 30-MAR-2000; 2000WO-US008439.
PR 15-MAY-2000; 2000WO-US013358.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 11-AUG-2000; 2000WO-US022031.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000WO-US030952.
PR 01-DEC-2000; 2000WO-US032678.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-JUN-2001; 2001WO-US017800.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 28-AUG-2001; 2001US-00941992.

(GETH) GENENTECH INC.

PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
PI Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi JC, Gurney AL, Kljavin IJ, Napier MA, Pan J, Paoni NP;
PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;
PI Zhang Z;

DR WPI; 2003-288105/28.
DR P-PSDB; ABU60598.

PT New transmembrane polypeptides and nucleic acids encoding the
PT polypeptides, useful in gene therapy, in chromosome identification, as
PT chromosome markers, or in generating probes.

XX Claim 2; Fig 277; 650pp; English.

XX The invention discloses isolated PRO secreted/transmembrane polypeptides
CC comprising a sequence without signal peptide and the nucleic acid
CC encoding them. The polypeptides can be used to raise antibodies that
CC specifically bind to the PRO polypeptide, for linking a bioactive
CC molecule to a cell expressing a PRO protein and for modulating at least
CC one biological activity of a cell. The PRO polypeptides or
CC polynucleotides are also useful in gene therapy, in chromosome
CC identification, as chromosome markers, or in generating probes. The PRO
CC polypeptides are useful as molecular markers for protein electrophoresis.

OS Homo sapiens.
XX US2003004311-A1.
PN
XX
PD 02-JAN-2003.
XX
PF 19-DEC-2001; 2001US-00028072.
XX
PR 18-JUN-1997; 97US-0049911P.
PR 26-AUG-1997; 97US-0056974P.
PR 17-SEP-1997; 97US-0059113P.
PR 17-SEP-1997; 97US-0059115P.
PR 17-SEP-1997; 97US-0059117P.
PR 17-SEP-1997; 97US-0059122P.
PR 17-SEP-1997; 97US-0059184P.
PR 18-SEP-1997; 97US-0059263P.
PR 19-SEP-1997; 97US-0059352P.
PR 19-SEP-1997; 97US-0059588P.
PR 24-SEP-1997; 97US-0059836P.
PR 17-OCT-1997; 97US-0062250P.
PR 17-OCT-1997; 97US-0062285P.
PR 17-OCT-1997; 97US-0062287P.
PR 17-OCT-1997; 97US-0063755P.
PR 24-OCT-1997; 97US-0062814P.
PR 24-OCT-1997; 97US-0062816P.
PR 24-OCT-1997; 97US-0063045P.
PR 24-OCT-1997; 97US-0063082P.
PR 24-OCT-1997; 97US-0063127P.
PR 27-OCT-1997; 97US-0063327P.
PR 28-OCT-1997; 97US-0063550P.
PR 28-OCT-1997; 97US-0063561P.
PR 29-OCT-1997; 97US-0063704P.
PR 29-OCT-1997; 97US-0063733P.
PR 29-OCT-1997; 97US-0063735P.
PR 29-OCT-1997; 97US-0063738P.
PR 03-NOV-1997; 97US-0064248P.
PR 07-NOV-1997; 97US-0064809P.
PR 12-NOV-1997; 97US-0065186P.
PR 17-NOV-1997; 97US-0065846P.
PR 21-NOV-1997; 97US-0066364P.
PR 24-NOV-1997; 97US-0066453P.
PR 24-NOV-1997; 97US-0066511P.
PR 24-NOV-1997; 97US-0066770P.
PR 11-DEC-1997; 97US-0069212P.
PR 11-DEC-1997; 97US-0069278P.
PR 11-DEC-1997; 97US-0069334P.
PR 16-DEC-1997; 97US-0069694P.
PR 23-JAN-1998; 98US-0072320P.
PR 04-FEB-1998; 98US-0073612P.
PR 09-FEB-1998; 98US-0074086P.
PR 09-FEB-1998; 98US-0074092P.
PR 12-MAR-1998; 98US-0077791P.
PR 20-MAR-1998; 98US-0078910P.
PR 25-MAR-1998; 98US-0079294P.
PR 27-MAR-1998; 98US-0079663P.
PR 27-MAR-1998; 98US-0079728P.
PR 31-MAR-1998; 98US-0080165P.
PR 12-JUN-1998; 98WO-US012456.
PR 14-JUL-1998; 98WO-US014552.
PR 28-AUG-1998; 98WO-US017888.
PR 10-SEP-1998; 98WO-US018824.
PR 14-SEP-1998; 98WO-US019093.
PR 14-SEP-1998; 98WO-US019094.
PR 14-SEP-1998; 98WO-US019177.
PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98WO-US019437.
PR 07-OCT-1998; 98WO-US021141.
PR 29-OCT-1998; 98WO-US022991.
PR 29-OCT-1998; 98WO-US022992.
PR 20-NOV-1998; 98WO-US024855.
PR 01-DEC-1998; 98WO-US025108.
PR 05-JAN-1999; 99WO-US000106.

PR 08-MAR-1999; 99WO-US005028.
PR 10-MAR-1999; 99WO-US005190.
PR 20-APR-1999; 99WO-US008615.
PR 14-MAY-1999; 99WO-US010733.
PR 02-JUN-1999; 99WO-US012252.
PR 01-SEP-1999; 99WO-US020111.
PR 08-SEP-1999; 99WO-US020594.
PR 13-SEP-1999; 99WO-US020944.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 05-OCT-1999; 99WO-US023089.
PR 29-NOV-1999; 99WO-US028214.
PR 30-NOV-1999; 99WO-US028313.
PR 30-NOV-1999; 99WO-US028409.
PR 01-DEC-1999; 99WO-US028301.
PR 01-DEC-1999; 99WO-US028634.
PR 02-DEC-1999; 99WO-US028551.
PR 02-DEC-1999; 99WO-US028564.
PR 02-DEC-1999; 99WO-US028565.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 30-DEC-1999; 99WO-US031243.
PR 30-DEC-1999; 99WO-US031274.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000277.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 18-FEB-2000; 2000WO-US004342.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US004914.
PR 24-FEB-2000; 2000WO-US005004.
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005746.
XX
PA
XX
XX
PI Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;
PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
XX WPI; 2003-352836/33.
DR P-PSDB; ABUS1110.
DR
XX
PT New isolated PRO polypeptide useful for treating diabetes, rheumatoid
PT arthritis, sports injuries, obesity, hearing loss in mammals, stroke, or
PT heart attack.
XX
PS Claim 2; Fig 481; 643pp; English.
XX
CC The present invention relates to the isolation of novel human PRO
CC polypeptides, and the polynucleotide sequences encoding them. The PRO
CC polypeptides are secreted and transmembrane proteins. The PRO
CC polypeptides and polynucleotides are useful for preparing a medicament
CC useful in the treatment of diabetes, bone and/or cartilage disorders
CC (e.g. rheumatoid arthritis, sports injuries, osteoarthritis), obesity,
CC hyper- or hypo-insulinaemia, hearing loss, and coagulation disorders
CC (e.g. stroke, heart attack). Anti-PRO antibodies are useful in diagnostic
CC assays for PRO, by detecting its expression in specific cells, tissues or
CC serum, and for affinity purification of PRO from recombinant cell culture
CC or natural sources. ACA66994-ACA67268 represent cDNA sequences encoding
CC the human PRO polypeptides of the invention. Note: The sequence data for
CC this patent was obtained in electronic format directly from the USPTO web
CC site at seqdata.uspto.gov/psipSIDEntry.html
XX
SQ Sequence 1346 BP; 457 A; 245 C; 237 G; 407 T; 0 U; 0 Other;

{GETH } GENENTECH INC.

Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;
Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;

WPI; 2003-352836/33.

P-PSDB; ABUS1110.

New isolated PRO polypeptide useful for treating diabetes, rheumatoid
arthritis, sports injuries, obesity, hearing loss in mammals, stroke, or
heart attack.

Claim 2; Fig 481; 643pp; English.

The present invention relates to the isolation of novel human PRO
polypeptides, and the polynucleotide sequences encoding them. The PRO
polypeptides are secreted and transmembrane proteins. The PRO
polypeptides and polynucleotides are useful for preparing a medicament
useful in the treatment of diabetes, bone and/or cartilage disorders
(e.g. rheumatoid arthritis, sports injuries, osteoarthritis), obesity,
hyper- or hypo-insulinaemia, hearing loss, and coagulation disorders
(e.g. stroke, heart attack). Anti-PRO antibodies are useful in diagnostic
assays for PRO, by detecting its expression in specific cells, tissues or
serum, and for affinity purification of PRO from recombinant cell culture
or natural sources. ACA66994-ACA67268 represent cDNA sequences encoding
the human PRO polypeptides of the invention. Note: The sequence data for
this patent was obtained in electronic format directly from the USPTO web
site at seqdata.uspto.gov/psipSIDEntry.html

Sequence 1346 BP; 457 A; 245 C; 237 G; 407 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	1.26e-123	Length:	1346
Score:	1102.00	Matches:	212
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0

Query Match:	100.00%	Indels:	0
DB:	7	Gaps:	0
US-09-989-724-387 (1-212) x ACA67234 (1-1346)			
Qy	1	MetLeuTrpLeuLeuPhePheLeuValThrAlaIleHisAlaGluLeuCysGlnProGly	20
Db	7	ATGTGTGGCTGCTCTTTTCTGGTGACTGCCATTCATGCTGAACCTCTGTCAACCAAGGT	66
Qy	21	AlaGluAsnAlaPheLysValArgLeuSerIleArgThrAlaLeuGlyAspLysAlaTyr	40
Db	67	GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT	126
Qy	41	AlaTrpAspThrAsnGluGluTyrLeuPheLysAlaMetValAlaPheSerMetArgLys	60
Db	127	GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTCTCCATGAGAAA	186
Qy	61	ValProAsnArgGluAlaThrGluIleSerHisValLeuLeuCysAsnValThrGlnArg	80
Db	187	GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCTACTTTGCAATGTAACCCAGAGG	246
Qy	81	ValSerPheTrpPheValValThrAspProSerLysAsnHisThrLeuProAlaValGlu	100
Db	247	GTATCATTTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCTCTGCTGTGAG	306
Qy	101	ValGlnSerAlaIleArgMetAsnLysAsnArgIleAsnAsnAlaPhePheLeuAsnAsp	120
Db	307	GTGCAATCAGCCATAAGAATGAACAAGACCGGATCAACAATGCCTTCTTTCTAAATGAC	366
Qy	121	GlnThrLeuGluPheLeuLysIleProSerThrLeuAlaProProMetAspProSerVal	140
Db	367	CAAACTCTGGAAATTTTAAAAATFCCCTTCCACACTGCACCACCCATGGACCCATCTGTG	426
Qy	141	ProIleTrpIleIleIlePheGlyValIlePheCysIleIleIleValAlaIleAlaLeu	160
Db	427	CCCATCTGGATTATTATATTGGTGTGATATTTGGTCATCATCATAGTTGCAATTGCACTA	486
Qy	161	LeuIleLeuSerGlyIleTrpGlnArgArgArgLysAsnLysGluProSerGluValAsp	180
Db	487	CTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACCAACCATCTGAAGTGGAT	546
Qy	181	AspAlaGluAspLysCysGluAsnMetIleThrIleGluAsnGlyIleProSerAspPro	200
Db	547	GACGCTGAAGATAAGTGTGAAACACATGATCACAATTGAAAATGGCATCCCTCTGTATCCC	606
Qy	201	LeuAspMetLysGlyGlyIleLeuMetMetProSer	212
Db	607	CTGGACATGAAGGGGGGCATATTATGATGCCTTCA	642
RESULT 13			
ACA64416			
ID	ACA64416	standard; cDNA; 1346 BP.	
XX	XX		
AC	ACA64416;		
XX	XX		
DT	17-JUN-2003	(first entry)	
DE	XX		
DE	XX	Novel human secreted and transmembrane protein PRO1312 cDNA.	
XX	XX		
KW	KW	Human; secreted and transmembrane protein; cytostatic; anti-HIV;	
KW	KW	virucide; hepatotropic; antiinflammatory; neuroprotective; gene therapy;	
KW	KW	PRO; pharmaceutical; diagnostic; biosensor; bioreactor; malignancy;	
KW	KW	cancer; ovarian cancer; colorectal cancer; Kaposi's sarcoma; leukaemia;	
KW	KW	lymphoma; hepatitis B; multiple sclerosis; Crohn's disease;	
KW	KW	drug screening; gene; ss.	
XX	OS	Homo sapiens.	
XX	XX		
PN	PN	US2003003531-A1.	
XX	XX		
PD	PD	02-JAN-2003.	
XX	XX		
PF	PF	19-NOV-2001; 2001US-00989734.	

XX	16-JUN-1997;	97US-0049787P.
PR	17-OCT-1997;	97US-0062250P.
PR	05-NOV-1997;	97WO-US020069.
PR	12-NOV-1997;	97US-0065186P.
PR	13-NOV-1997;	97US-0065311P.
PR	24-NOV-1997;	97US-0066770P.
PR	25-FEB-1998;	98US-0075945P.
PR	20-MAR-1998;	98US-0078910P.
PR	28-APR-1998;	98US-0083322P.
PR	07-MAY-1998;	98US-0084600P.
PR	28-MAY-1998;	98US-0087106P.
PR	02-JUN-1998;	98US-0087607P.
PR	02-JUN-1998;	98US-0087609P.
PR	02-JUN-1998;	98US-0087759P.
PR	03-JUN-1998;	98US-0087827P.
PR	04-JUN-1998;	98US-0088021P.
PR	04-JUN-1998;	98US-0088025P.
PR	04-JUN-1998;	98US-0088026P.
PR	04-JUN-1998;	98US-0088028P.
PR	04-JUN-1998;	98US-0088029P.
PR	04-JUN-1998;	98US-0088030P.
PR	04-JUN-1998;	98US-0088033P.
PR	04-JUN-1998;	98US-0088326P.
PR	05-JUN-1998;	98US-0088167P.
PR	05-JUN-1998;	98US-0088202P.
PR	05-JUN-1998;	98US-0088212P.
PR	05-JUN-1998;	98US-0088217P.
PR	09-JUN-1998;	98US-0088655P.
PR	10-JUN-1998;	98US-0088734P.
PR	10-JUN-1998;	98US-0088738P.
PR	10-JUN-1998;	98US-0088742P.
PR	10-JUN-1998;	98US-0088810P.
PR	10-JUN-1998;	98US-0088824P.
PR	10-JUN-1998;	98US-0088826P.
PR	11-JUN-1998;	98US-0088858P.
PR	11-JUN-1998;	98US-0088861P.
PR	11-JUN-1998;	98US-0088876P.
PR	12-JUN-1998;	98US-0089105P.
PR	16-JUN-1998;	98US-0089440P.
PR	16-JUN-1998;	98US-0089512P.
PR	16-JUN-1998;	98US-0089514P.
PR	17-JUN-1998;	98US-0089532P.
PR	17-JUN-1998;	98US-0089538P.
PR	17-JUN-1998;	98US-0089598P.
PR	17-JUN-1998;	98US-0089599P.
PR	17-JUN-1998;	98US-0089600P.
PR	17-JUN-1998;	98US-0089653P.
PR	18-JUN-1998;	98US-0089801P.
PR	18-JUN-1998;	98US-0089907P.
PR	18-JUN-1998;	98US-0089908P.
PR	16-SEP-1998;	98WO-US019330.
PR	17-SEP-1998;	98WO-US019437.
PR	07-OCT-1998;	98WO-US021141.
PR	01-DEC-1998;	98WO-US025108.
PR	05-JAN-1999;	99WO-US000106.
PR	08-MAR-1999;	99WO-US005028.
PR	02-JUN-1999;	99WO-US012252.
PR	15-SEP-1999;	99WO-US021090.
PR	15-SEP-1999;	99WO-US021547.
PR	30-NOV-1999;	99WO-US028313.
PR	01-DEC-1999;	99WO-US028301.
PR	01-DEC-1999;	99WO-US028634.
PR	16-DEC-1999;	99WO-US030095.
PR	20-DEC-1999;	99WO-US030911.
PR	05-JAN-2000;	2000WO-US000219.
PR	06-JAN-2000;	2000WO-US000376.
PR	11-FEB-2000;	2000WO-US003565.
PR	18-FEB-2000;	2000WO-US004341.
PR	22-FEB-2000;	2000WO-US004414.
PR	24-FEB-2000;	2000WO-US004914.
PR	24-FEB-2000;	2000WO-US005004.
PR	02-MAR-2000;	2000WO-US005841.

PR 10-MAR-2000; 2000WO-US006319.
PR 15-MAR-2000; 2000WO-US006884.
PR 20-MAR-2000; 2000WO-US007377.
PR 30-MAR-2000; 2000WO-US008439.
PR 15-MAY-2000; 2000WO-US013358.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 11-AUG-2000; 2000WO-US022031.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000WO-US030952.
PR 01-DEC-2000; 2000WO-US032678.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-JUN-2001; 2001WO-US017800.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 28-AUG-2001; 2001US-00941992.
XX
PA (GETH) GENENTECH INC.
XX
PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
PI Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi JC, Gurney AL, Kljavin IJ, Napier MA, Pan J, Paoni NF;
PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;
PI Zhang Z;
XX
DR WPI; 2003-352829/33.
DR P-PSDB; ABU72565.
XX
PT New genes and secreted and transmembrane polypeptides (e.g. PRO183 or
PT PRO184), useful for treating or diagnosing e.g. ovarian cancer, Kaposi's
PT sarcoma, leukemia, lymphoma, hepatitis B, multiple sclerosis or Crohn's
PT disease.
XX
PS Claim 1: Fig 277; 663pp; English.
XX
CC The invention describes a new isolated nucleic acid molecule comprising
CC the full length coding sequence of the DNA deposited with the American
CC Type Culture Collection (e.g. ATCC Deposit No. 209621, 552-PTA, 819-PTA,
CC 209439, 203135, etc); or a sequence with at least 80% identity to a DNA
CC encoding a PRO polypeptide. The PRO polypeptides or polynucleotides are
CC useful as pharmaceuticals, diagnostics, biosensors or bioreactors. These
CC are particularly useful for detecting or treating e.g. malignancies or
CC cancers (e.g. ovarian cancer, colorectal cancer, Kaposi's sarcoma,
CC leukaemia or lymphoma), hepatitis B, multiple sclerosis, or Crohn's
CC disease in mammals. The PRO polypeptides are useful in drug screening,
CC particularly as targets for therapeutic intervention in these diseases,
CC and in the diagnostic determination of the presence of these diseases.
CC The PRO polypeptides are also useful as molecular weight markers, or for
CC chromosome identification. The PRO genes are useful as hybridisation
CC probes, or for screening libraries of human cDNA, genomic DNA or mRNA.
CC The PRO genes may also be used in gene therapy, particularly for
CC replacing a defective gene. This sequence encodes a novel human secreted
CC and transmembrane PRO polypeptide
XX
SQ Sequence 1346 BP; 457 A; 245 C; 237 G; 407 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 1.26e-123 Length: 1346
Score: 1102.00 Matches: 212
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 7 Gaps: 0

US-09-989-724-387 (1-212) x ACA64416 (1-1346)

Qy 1 MetLeuTrpLeuPhePheLeuValThrAlaIleHisAlaGluLeuCysGlnProGly 20
|||||

Db 7 ATGTTGTGGCTGCTCTTTTTTCTGTGACTGCCATTGCTGAACTCTGTCAACACAGGT 66
Qy 21 AlaGluAsnAlaPheLysValArgLeuSerIleArgThrAlaLeuGlyAspLysAlaTyr 40
|||||
Db 67 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 126
Qy 41 AlaTrpAspThrAsnGluGluTyLeuPheLysAlaMetValAlaPheSerMetArgLys 60
|||||
Db 127 GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAA 186
Qy 61 ValProAsnArgGluAlaThrGluIleSerHisValLeuLeuCysAsnValThrGlnArg 80
|||||
Db 187 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCTTACTTTGCAATGTAACCCAGAG 246
Qy 81 ValSerPheTrpPheValValThrAspProSerLysAsnHisThrLeuProAlaValGlu 100
|||||
Db 247 GTATCATTTCTGGTTTGTGTTACAGACCTTTCAAAAAATCACACCTTCCTGCTGTGAG 306
Qy 101 ValGlnSerAlaIleArgMetAsnLysAsnArgIleAsnAsnAlaPhePheLeuAsnAsp 120
|||||
Db 307 GTGCAANTCAGCCATAAGAATGAAGAAGACCGGATCAACAAATGCCTTCTTTCTAAATGAC 366
Qy 121 GlnThrLeuGluPheLeuLysIleProSerThrLeuAlaProProMetAspProSerVal 140
|||||
Db 367 CAAACTCTGGAATTTTAAAAATCCCTTCCACACTTGCACCCATGGACCCATCTGTG 426
Qy 141 ProIleTrpIleIlePheGlyValIlePheCysIleIleIleValAlaIleAlaLeu 160
|||||
Db 427 CCCATCTGGATTATTATATTGTTGTGATATTTTGCATCATCATAGTTGCAATTGCACTA 486
Qy 161 LeuIleLeuSerGlyIleTrpGlnArgArgArgLysAsnLysGluProSerGluValAsp 180
|||||
Db 487 CTGATTTTATCAGGGATCTGGCAACGTAGAGAAGAAACAAGAACCATCTGAAGTGGAT 546
Qy 181 AspAlaGluAspLysCysGluAsnMetIleThrIleGluAsnGlyIleProSerAspPro 200
|||||
Db 547 GACGCTGAAGATAAGTGTGAAAACATGATCAACAATTGAAAATGGCATCCCTCTGATCCC 606
Qy 201 LeuAspMetLysGlyGlyIleLeuMetMetProSer 212
|||||
Db 607 CTGGACATGAAGGGGGGCATATTATTAATGATGCCTTCA 642

RESULT 14
ACA03843
ID ACA03843 standard; cDNA; 1346 BP.
XX
AC ACA03843;
XX
DT 23-MAY-2003 (first entry)
XX
DE cDNA encoding human PRO polypeptide #241.
XX
KW Human; PRO polypeptide; secreted and transmembrane protein;
KW tumour necrosis factor-alpha; TNF-alpha; blood; proliferation;
KW differentiation; chondrocyte; tumour; genetic disorder; cytostatic; gene;
KW ss.
XX
OS Homo sapiens.
XX
PN US2003036180-A1.
XX
PD 20-FEB-2003.
XX
PF 09-MAY-2002; 2002US-00143114.
XX
PR 31-MAR-1997; 97WO-US005230.
PR 12-JUN-1998; 98WO-US012456.
PR 14-JUL-1998; 98WO-US014552.
PR 28-AUG-1998; 98WO-US017888.
PR 10-SEP-1998; 98WO-US018824.
PR 14-SEP-1998; 98WO-US019093.
PR 14-SEP-1998; 98WO-US019094.
PR 14-SEP-1998; 98WO-US019177.

PR 16-SEP-1998; 98WO-US019330.
 PR 17-SEP-1998; 98WO-US019437.
 PR 07-OCT-1998; 98WO-US021141.
 PR 29-OCT-1998; 98WO-US022991.
 PR 29-OCT-1998; 98WO-US022992.
 PR 20-NOV-1998; 98WO-US024855.
 PR 01-DEC-1998; 98WO-US025108.
 PR 05-JAN-1999; 99WO-US000106.
 PR 08-MAR-1999; 99WO-US005028.
 PR 10-MAR-1999; 99WO-US005190.
 PR 20-APR-1999; 99WO-US008615.
 PR 14-MAY-1999; 99WO-US010733.
 PR 02-JUN-1999; 99WO-US012252.
 PR 01-SEP-1999; 99WO-US020111.
 PR 08-SEP-1999; 99WO-US020594.
 PR 13-SEP-1999; 99WO-US020944.
 PR 15-SEP-1999; 99WO-US021090.
 PR 15-SEP-1999; 99WO-US021547.
 PR 05-OCT-1999; 99WO-US023089.
 PR 29-NOV-1999; 99WO-US028214.
 PR 30-NOV-1999; 99WO-US028313.
 PR 30-NOV-1999; 99WO-US028409.
 PR 01-DEC-1999; 99WO-US028301.
 PR 01-DEC-1999; 99WO-US028634.
 PR 02-DEC-1999; 99WO-US028551.
 PR 02-DEC-1999; 99WO-US028564.
 PR 02-DEC-1999; 99WO-US028565.
 PR 16-DEC-1999; 99WO-US030095.
 PR 20-DEC-1999; 99WO-US030911.
 PR 20-DEC-1999; 99WO-US030999.
 PR 22-DEC-1999; 99WO-US030720.
 PR 30-DEC-1999; 99WO-US031243.
 PR 30-DEC-1999; 99WO-US031274.
 PR 05-JAN-2000; 2000WO-US000219.
 PR 06-JAN-2000; 2000WO-US000277.
 PR 06-JAN-2000; 2000WO-US000376.
 PR 11-FEB-2000; 2000WO-US003565.
 PR 18-FEB-2000; 2000WO-US004341.
 PR 18-FEB-2000; 2000WO-US004342.
 PR 22-FEB-2000; 2000WO-US004414.
 PR 24-FEB-2000; 2000WO-US004914.
 PR 24-FEB-2000; 2000WO-US005004.
 PR 01-MAR-2000; 2000WO-US005601.
 PR 02-MAR-2000; 2000WO-US005746.
 PR 10-MAR-2000; 2000WO-US006319.
 PR 15-MAR-2000; 2000WO-US006884.
 PR 20-MAR-2000; 2000WO-US007377.
 PR 21-MAR-2000; 2000WO-US007532.
 PR 30-MAR-2000; 2000WO-US008439.
 PR 17-MAY-2000; 2000WO-US013705.
 PR 22-MAY-2000; 2000WO-US014042.
 PR 30-MAY-2000; 2000WO-US014941.
 PR 02-JUN-2000; 2000WO-US015264.
 PR 28-JUL-2000; 2000WO-US020710.
 PR 11-AUG-2000; 2000WO-US022031.
 PR 23-AUG-2000; 2000WO-US023522.
 PR 24-AUG-2000; 2000WO-US023328.
 PR 08-NOV-2000; 2000WO-US030952.
 PR 10-NOV-2000; 2000WO-US030873.
 PR 01-DEC-2000; 2000WO-US032678.
 PR 20-DEC-2000; 2000US-00747259.
 PR 28-FEB-2001; 2000WO-US034956.
 PR 28-FEB-2001; 2001US-00796498.
 PR 01-MAR-2001; 2001WO-US006520.
 PR 09-MAR-2001; 2001WO-US006666.
 PR 14-MAR-2001; 2001US-00802706.
 PR 22-MAR-2001; 2001US-00816744.
 PR 05-APR-2001; 2001US-00828366.
 PR 10-MAY-2001; 2001US-00854208.
 PR 10-MAY-2001; 2001US-00854280.
 PR 18-MAY-2001; 2001US-00860216.

PR 25-MAY-2001; 2001US-00866028.
 PR 25-MAY-2001; 2001US-00866034.
 PR 25-MAY-2001; 2001WO-US017092.
 PR 01-JUN-2001; 2001US-00872035.
 PR 01-JUN-2001; 2001WO-US017800.
 PR 05-JUN-2001; 2001US-00874503.
 PR 14-JUN-2001; 2001US-00882636.
 PR 19-JUN-2001; 2001US-00886342.
 PR 20-JUN-2001; 2001WO-US019692.
 PR 21-JUN-2001; 2001US-00887879.
 PR 22-JUN-2001; 2001WO-US020116.
 PR 29-JUN-2001; 2001WO-US021066.
 PR 09-JUL-2001; 2001WO-US021735.
 PR 18-JUL-2001; 2001US-00908827.
 PR 06-AUG-2001; 2001US-00924419.
 PR 09-AUG-2001; 2001US-00927796.
 PR 16-AUG-2001; 2001US-00931836.
 PR 19-DEC-2001; 2001US-00028072.

(GETH) GENENTECH INC.

PI Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;
 PI Gerritsen MB, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
 PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;

DR WPI; 2003-332040/31.
 DR P-PSDB; ABU66810.

XX New secreted and transmembrane PRO nucleic acids, useful for gene
 therapy, in chromosome and gene mapping, as chromosome markers, in tissue
 typing, and in chromosome identification.

PS Claim 2; Fig 481; 660pp; English.

XX The present invention relates to the isolation of novel human PRO
 CC polypeptides, and the polynucleotide sequences encoding them. The PRO
 CC polypeptides are secreted and transmembrane proteins. The PRO
 CC polypeptides are useful for detecting other PRO polypeptides, for linking
 CC bioactive molecules to cells expressing PRO polypeptides, and for
 CC biological activities of cells expressing PRO polypeptides, and for
 CC identifying agonists or antagonists. The PRO polypeptides are useful for
 CC for stimulating the release of tumour necrosis factor (TNF)-alpha from
 CC human blood, for stimulating the proliferation or differentiation of
 CC chondrocytes, and detecting the presence of tumours. The polynucleotide
 CC sequences encoding PRO polypeptides are useful as hybridisation probes,
 CC in chromosome and gene mapping, in the generation of antisense RNA and
 CC DNA, in the preparation of PRO polypeptides, for generating transgenic
 CC animals or knockout animals, for the genetic analysis of individuals with
 CC genetic disorders, and in gene therapy. ACA03603-ACA03877 represent cDNAs
 CC encoding the human PRO polypeptides of the invention. Note: The sequence
 CC data for this patent was obtained in electronic format directly from the
 CC USPTO web site at seqdata.uspto.gov/psipsDIDentry.html

SQ Sequence 1346 BP; 457 A; 245 C; 237 G; 407 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 1.26e-123 Length: 1346
 Score: 1102.00 Matches: 212
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 7 Gaps: 0

US-09-989-724-387 (1-212) x ACA03843 (1-1346)

Qy 1 MetLeuTrpLeuLeuPheLeuValThrAlaIleHiaGluLeuCysGlnProGly 20
 |||||
 Db 7 ATGTTGGCTGCTCTCTTTTCTGGTGACTGCCATTCATCTGCTGCAACAGGT 66
 Qy 21 AlaGluAsnAlaPheLysValArgLeuSerIleArgThrAlaLeuGlyAspLysAlaTyr 40
 |||||
 Db 67 GCAGAAATGCTTTTAAAGTGAGACTTAGTAGTATCAGAACACAGCTCTGGGAGATAAGCATAT 126

QY 41 AlaTrpAspThrAsnGluGluTyrLeuPheLysAlaMetValAlaPheSerMetArgLys 60
DB 127 GCTGGGATACCAATGAAGAAATACCTCTTCAAAGCGATGGTAGCTTCTCCATGAGAAA 186
QY 61 ValProAsnArgGluAlaThrGluIleSerHisValLeuLeuCysAsnValThrGlnArg 80
DB 187 GTTCCCAACAGAGAGCAACAGAAATTTCCCATGTCTCTACTTTGCAATGTAAACCGAGG 246
QY 81 ValSerPheTrpPheValValThrAspProSerLysAsnHisThrLeuProAlaValGlu 100
DB 247 GTATCATTTCTGGTTTGTGGTTACAGACCTTCAAAAAATCACACCTTCTCTGCTGTGAG 306
QY 101 ValGlnSerAlaIleArgMetAsnLysAsnArgIleAsnAsnAlaPhePheLeuAsnAsp 120
DB 307 GTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGAC 366
QY 121 GlnThrLeuGluPheLeuLysIleProSerThrLeuAlaProProMetAspProSerVal 140
DB 367 CAAACTCTGGAATTTTAAAAATCCCTTCCCACTTGCAACCCATGCACCATCTGTG 426
QY 141 ProIleTrpIleIleIlePheGlyValIlePheCysIleIleIleValAlaIleAlaLeu 160
DB 427 CCCATCTGGATTATATATTTGGTGTGATATTTGCATCATCATAGTTGCAATGCACTA 486
QY 161 LeuIleLeuSerGlyIleTrpGlnArgArgArgLysAsnLysGluProSerGluValAsp 180
DB 487 CTGATTTATCAGGGATCTGGCAACGTAGAGAAGAAACAAGAACCATCTGAAGTGGAT 546
QY 181 AspAlaGluAspLysCysGluAsnMetIleThrIleGluAsnGlyIleProSerAspPro 200
DB 547 GACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCTCTGATCCC 606
QY 201 LeuAspMetLysGlyGlyIleLeuMetMetProSer 212
DB 607 CTGGACATGAAGGGGGCATATTAAATGATGCCTTCA 642

RESULT 15

ABX89381
ID ABX89381 standard; cDNA; 1346 BP.
XX
AC ABX89381;
DT 13-MAY-2003 (first entry)
XX
DE DNA encoding novel secreted and transmembrane protein PRO1312.
KW Human; PRO; hypertrophy of neonatal heart; angiogenesis; wound healing;
KW cardiac insufficiency disorder; cancer; tumour; immune response;
KW adrenal cortical capillary endothelial growth; c-fos induction;
KW vascular endothelial growth factor inhibition; VEGF inhibition;
KW endothelial cell growth inhibitor; T-lymphocytes stimulation;
KW retinal neurons cell survival; rod photoreceptor cell survival;
KW retinal disorder; retinitis pigmentosa; kidney disease;
KW mammalian kidney mesangial cell proliferation; Berger disease;
KW dermatitis; herpeticiformis; Crohn's disease; chondrocyte proliferation;
KW chondrocyte redifferentiation; sports injury; arthritis; gene; ss.
XX
OS Homo sapiens.
XX
PN US2003017563-A1.
XX
PD 23-JAN-2003.
XX
PF 07-MAY-2002; 2002US-00140808.
XX
PR 31-MAR-1997; 97WO-US005230.
PR 12-JUN-1998; 98WO-US012456.
PR 14-JUL-1998; 98WO-US014552.
PR 28-AUG-1998; 98WO-US017888.
PR 10-SEP-1998; 98WO-US018824.
PR 14-SEP-1998; 98WO-US019093.
PR 14-SEP-1998; 98WO-US019094.
PR 14-SEP-1998; 98WO-US019177.

PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98WO-US019437.
PR 07-OCT-1998; 98WO-US021141.
PR 29-OCT-1998; 98WO-US022991.
PR 29-OCT-1998; 98WO-US022992.
PR 20-NOV-1998; 98WO-US024855.
PR 01-DEC-1998; 98WO-US025108.
PR 05-JAN-1999; 99WO-US000106.
PR 08-MAR-1999; 99WO-US005028.
PR 10-MAR-1999; 99WO-US005190.
PR 20-APR-1999; 99WO-US008615.
PR 14-MAY-1999; 99WO-US010733.
PR 02-JUN-1999; 99WO-US012252.
PR 01-SEP-1999; 99WO-US020111.
PR 08-SEP-1999; 99WO-US020594.
PR 13-SEP-1999; 99WO-US020944.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 05-OCT-1999; 99WO-US023089.
PR 29-NOV-1999; 99WO-US028214.
PR 30-NOV-1999; 99WO-US028313.
PR 30-NOV-1999; 99WO-US028409.
PR 01-DEC-1999; 99WO-US028301.
PR 01-DEC-1999; 99WO-US028634.
PR 02-DEC-1999; 99WO-US028551.
PR 02-DEC-1999; 99WO-US028564.
PR 02-DEC-1999; 99WO-US028565.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 20-DEC-1999; 99WO-US030999.
PR 22-DEC-1999; 99WO-US030720.
PR 30-DEC-1999; 99WO-US031243.
PR 30-DEC-1999; 99WO-US031274.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000277.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 18-FEB-2000; 2000WO-US004342.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US004914.
PR 24-FEB-2000; 2000WO-US005004.
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005746.
PR 02-MAR-2000; 2000WO-US005841.
PR 10-MAR-2000; 2000WO-US006319.
PR 15-MAR-2000; 2000WO-US006884.
PR 20-MAR-2000; 2000WO-US007377.
PR 21-MAR-2000; 2000WO-US007532.
PR 30-MAR-2000; 2000WO-US008439.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 11-AUG-2000; 2000WO-US022031.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000WO-US030952.
PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000US-00747259.
PR 28-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001US-00796498.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-MAR-2001; 2001WO-US006666.
PR 09-MAR-2001; 2001US-00802706.
PR 14-MAR-2001; 2001US-00808689.
PR 22-MAR-2001; 2001US-00816744.
PR 05-APR-2001; 2001US-00828366.
PR 10-MAY-2001; 2001US-00854208.
PR 10-MAY-2001; 2001US-00854280.
PR 18-MAY-2001; 2001US-00860216.

PR 25-MAY-2001; 2001US-00866028.
PR 25-MAY-2001; 2001US-00866034.
PR 25-MAY-2001; 2001WO-US017092.
PR 01-JUN-2001; 2001US-00872035.
PR 01-JUN-2001; 2001WO-US017800.
PR 05-JUN-2001; 2001US-00874503.
PR 14-JUN-2001; 2001US-00882636.
PR 19-JUN-2001; 2001US-00886342.
PR 20-JUN-2001; 2001WO-US019692.
PR 21-JUN-2001; 2001US-00887879.
PR 22-JUN-2001; 2001WO-US020116.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 18-JUL-2001; 2001US-00908627.
PR 06-AUG-2001; 2001US-00924419.
PR 09-AUG-2001; 2001US-00927796.
PR 16-AUG-2001; 2001US-00931836.
PR 19-DEC-2001; 2001US-00028072.
XX

PA (GETH) GENENTECH INC.

XX Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;
PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
XX WPI; 2003-148238/14.

DR P-PSDB; ABUS9891.

XX Two hundred and seventy five nucleic acids encoding PRO polypeptides,
PT useful for treating pericyte-associated tumors, diabetes and various bone
PT and/or cartilage disorders, e.g. arthritis.

XX Claim 2; Fig 481; 659pp; English.

CC The invention describes an isolated human PRO polypeptide. The PRO
CC polypeptides are useful in detecting PRO polypeptides in a sample, in
CC linking a bioactive molecule to a cell expressing a PRO polypeptide, and
CC in modulating at least one biological activity of a cell expressing a PRO
CC polypeptide. PRO1312 stimulates hypertrophy of neonatal heart and is thus
CC useful for treating cardiac insufficiency disorders. PRO1154 and PRO1186
CC stimulate adrenal cortical capillary endothelial growth, and PRO536,
CC PRO943, PRO828, PRO826, PRO1068 or PRO535, PRO826, PRO819, PRO1126,
CC PRO1360 and PRO1387 induce c-fos in endothelial cells, and are thus
CC useful for treating conditions or disorders where angiogenesis would be
CC beneficial, e.g. wound healing and antagonist of this polypeptide are
CC useful for treating cancerous tumours. PRO812 inhibits vascular
CC endothelial growth factor (VEGF) stimulated proliferation of endothelial
CC cells and is thus useful for inhibiting endothelial cell growth in
CC mammals which would be beneficial in inhibiting tumour growth. PRO826,
CC PRO1068, PRO1184, PRO1346 and PRO1375 stimulate proliferation of
CC stimulated T-lymphocytes and are therapeutically useful for enhancing
CC immune response. PRO828, PRO826, PRO1068 or PRO1132 enhance survival of
CC retinal neurons cells (PRO1132 is also enhances survival/proliferation of
CC rod photoreceptor cells) and therefore are useful for treating retinal
CC disorders of injuries, e.g. retinitis pigmentosa, AMD. PRO819, PRO813
CC and PRO11066 induce proliferation of mammalian kidney mesangial cells,
CC and therefore are useful for treating kidney disorders associated with
CC decreased mesangial cell function such as Berger disease or other
CC nephropathies associated with dermatitis, herpeticiformis or Crohn's
CC disease. PRO1310, PRO844, PRO1312, PRO1192 and PRO1387 induce the
CC proliferation and/or redifferentiation of chondrocytes in culture and are
CC thus useful for treating sports injuries, and arthritis. This sequence
CC encodes a novel human PRO protein

XX SQ Sequence 1346 BP; 457 A; 245 C; 237 G; 407 T; 0 U; 0 Other;

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US-09-989-724-387 (1-212) x ABX89381 (1-1346)

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Qy	21	AlaGluAsnAlaPheLysValArgLeuSerIleArgThrAlaLeuGlyAspLysAlaTyr	40
Db	67	GCAGAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT	126
Qy	41	AlaTrpAspThrAsnGluGluTyrLeuPheLysAlaMetValAlaPheSerMetArgLys	60
Db	127	GCCTGGGATACCAATGAAGATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA	186
Qy	61	ValProAsnArgGluAlaThrGluIleSerHisValLeuLeuCysAsnValThrGlnArg	80
Db	187	GTTCCCAACAGAGAAAGCAACAGAAATTTCCCATGTCTTCTTGAATGTAAACCCAGAGG	246
Qy	81	ValSerPheTrpPheValValThrAspProSerLysAsnHisThrLeuProAlaValGlu	100
Db	247	GTATCAATCTGGTTTGTGGTTACAGACCTTCAAAAAATCACACCTTCTCTGCTGTTGAG	306
Qy	101	ValGlnSerAlaIleArgMetAsnLysAsnArgIleAsnAsnAlaPhePheLeuAsnAsp	120
Db	307	GTGCAATCAGCCATAGAATGAACAGAACCCGGATCAACAATGCCCTTCTTCTTAATGAC	366
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Db	367	CAAACTCTGGAATTTTAAAAATCCCTTCCACACTTGCCACCACCCATGGACCCCATCTGTG	426
Qy	141	ProIleTrpIleIleIlePheGlyValIlePheCysIleIleIleValAlaIleAlaLeu	160
Db	427	CCCATCTGGATTATTATATTTTGGTGTGATATTTTGCATCATCATAGTTGCAATGCACTA	486
Qy	161	LeuIleLeuSerGlyIleTrpGlnArgArgArgLysAsnLysGluProSerGluValAsp	180
Db	487	CTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAAAGAACCAATCTGAAGTGGAT	546
Qy	181	AspAlaGluAspLysCysGluAsnMetIleThrIleGluAsnGlyIleProSerAspPro	200
Db	547	GACGCTGAAGATAAGTGTGAAACATGATCACAAATTGAAATGGCATCCCTCTGTATCCC	606
Qy	201	LeuAspMetLysGlyGlyIleLeuMetMetProSer	212
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GenCore version 5.1.6
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1041.147 Million cell updates/sec

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Delop 6.0 , Delext 7.0

Searched: 682709 seqs, 277475446 residues

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Minimum DB seq length: 0
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Maximum Match 100%
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	1064	96.6	848	4	US-09-663-600A-27
4	1064	96.6	848	4	US-09-621-976-5
5	376	34.1	2415	3	US-08-989-299-3
6	376	34.1	2415	4	US-09-407-427-3
7	376	34.1	3396	3	US-08-989-299-1
8	376	34.1	3396	4	US-10-158-847-141
9	376	34.1	3396	4	US-09-407-427-1
10	359	32.6	2920	4	US-10-158-847-137
11	281	25.5	862	3	US-09-289-349-6
12	233.5	21.2	2350	4	US-09-280-116-40

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	14	90	8.2	3136	1	US-08-188-228-41	Sequence 41, Appl
	15	90	8.2	3136	1	US-08-332-638-41	Sequence 41, Appl
	16	89.5	8.1	2550	1	US-08-188-228-53	Sequence 53, Appl
	17	89.5	8.1	2550	1	US-08-332-643-47	Sequence 47, Appl
	18	89.5	8.1	2550	1	US-08-332-638-53	Sequence 53, Appl
	19	89.5	8.1	3146	4	US-09-620-312D-277	Sequence 277, App
	20	86	7.8	3207	1	US-07-946-497-1	Sequence 1, Appli
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	23	85	7.7	4756	4	US-09-023-655-1461	Sequence 1461, Ap
	24	83.5	7.6	5117	3	US-08-854-585-1	Sequence 1, Appli
	25	83.5	7.6	5117	4	US-09-447-533-1	Sequence 1, Appli
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	29	82.5	7.5	1590	4	US-09-134-000C-2543	Sequence 2543, Ap
	30	81.5	7.4	5717	4	US-09-023-655-1333	Sequence 1333, Ap
	31	80	7.3	87563	4	US-09-453-702B-57	Sequence 57, Appl
	32	78.5	7.1	1761	4	US-09-404-879A-387	Sequence 387, App
	33	78.5	7.1	2608	4	US-09-404-879A-386	Sequence 386, App
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	45	76	6.9	1728	4	US-09-096-731A-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1

US-08-905-223-27
; Sequence 27, Application US/08905223
; Patent No. 6222029
; GENERAL INFORMATION:
; APPLICANT: Edwards, Jean-Baptiste D.
; APPLICANT: Duclert, Aymeric
; APPLICANT: Lacroix, Bruno
; TITLE OF INVENTION: 5' ESTS FOR SECRETED PROTEINS
; NUMBER OF SEQUENCES: 503
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson & Bear
; STREET: 501 West Broadway
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92101-3505
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Win95
; SOFTWARE: Word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/905,223
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Israelsen, Ned A.
; REGISTRATION NUMBER: 29,655
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 235-8550
; TELEFAX: (619) 235-0176
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 848 base pairs

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; TYPE: NUCLEIC ACID
; STRANDEDNESS: DOUBLE
; TOPOLOGY: LINEAR
; MOLECULE TYPE: CDNA
; ORGANISM: Homo Sapiens
; DEVELOPMENTAL STAGE: Fetal
; TISSUE TYPE: kidney
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 32..73
; IDENTIFICATION METHOD: Von Heijne matrix
; OTHER INFORMATION: score 10.7
; OTHER INFORMATION: seq LWLLFFLVTAIHA/EL
US-08-905-223-27
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Score: 1064.00 Matches: 208
Percent Similarity: 97.65% Conservativity: 0
Best Local Similarity: 97.65% Mismatches: 4
Query Match: 96.55% Indels: 1
DB: 3 Gaps: 0
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US-09-989-724-387 (1-212) x US-08-905-223-27 (1-848)

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QY 21 AlaGluAsnAlaPheLysValArgLeuSerIleArgThrAlaLeuGlyAspLysAlaTyr 40
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QY 41 AlaTrpAspThrAsnGluGluTyrLeuPheLysAlaMetValAlaPheSerMetArgLys 60
DB 152 GCCTGGGATACCAATGAAGAATACCTCTTCAAGCGATGGTAGCTTCTCCATGAGAAAA 211
QY 61 ValProAsnArgGluAlaThrGluIleSerHisValLeuLeuCysAsnValThrGlnArg 80
DB 212 GTTCCCAACAGAGAACCAAGAAATTTCCCATGTCTACTTTGCAATGTAACCCAGAGG 271
QY 81 ValSerPheTrpPheValValThrAspProSerLysAsnHisThrLeuProAlaValGlu 100
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QY 181 AspAlaGluAspLysCysGluAsnMetIleThrIleGluAsnGlyIleProSerAspPro 200
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RESULT 2

US-09-247-155-27

; Sequence 27, Application US/09247155A

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; Patent No. 6312922
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, Jean-Baptiste
; APPLICANT: Duclert, Aymeric
; APPLICANT: Bougueleret, Lydie
; TITLE OF INVENTION: Complementary DNAs
; FILE REFERENCE: GENSET.021A
; CURRENT APPLICATION NUMBER: US/09/247,155A
; CURRENT FILING DATE: 1999-02-09
; EARLIER APPLICATION NUMBER: 60/074,121
; EARLIER FILING DATE: 1998-02-09
; EARLIER APPLICATION NUMBER: 60/081,563
; EARLIER FILING DATE: 1998-04-13
; EARLIER APPLICATION NUMBER: 60/096,116
; EARLIER FILING DATE: 1998-08-10
; EARLIER APPLICATION NUMBER: 60/099,273
; EARLIER FILING DATE: 1998-10-04
; NUMBER OF SEQ ID NOS: 182
; SOFTWARE: Patent.pm
; SEQ ID NO 27
; LENGTH: 848
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 32..73
; OTHER INFORMATION: Von Heijne matrix
US-09-247-155-27
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Score: 1064.00 Matches: 208
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Best Local Similarity: 97.65% Mismatches: 4
Query Match: 96.55% Indels: 1
DB: 4 Gaps: 0
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US-09-989-724-387 (1-212) x US-09-247-155-27 (1-848)

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QY 21 AlaGluAsnAlaPheLysValArgLeuSerIleArgThrAlaLeuGlyAspLysAlaTyr 40
DB 92 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 151
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DB 152 GCCTGGGATACCAATGAAGAATACCTCTTCAAGCGATGGTAGCTTCTCCATGAGAAAA 211
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DB 212 GTTCCCAACAGAGAACCAAGAAATTTCCCATGTCTACTTTGCAATGTAACCCAGAGG 271
QY 81 ValSerPheTrpPheValValThrAspProSerLysAsnHisThrLeuProAlaValGlu 100
DB 272 GTATCATCTGGTTTGTGTTACAGACCTTCAAAAAATCACACCCTTCTGCTGTGTGAG 331
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QY 141 ProIleTrpIleIlePheGlyValIlePheCysIleIleIleValAlaIleAlaLeu 160
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RESULT 3
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; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, Jean-Baptiste
; APPLICANT: Duclert, Aymeric
; APPLICANT: Bougueleret, Lydie
; TITLE OF INVENTION: EXTENDED CDNAS FOR SECRETED PROTEINS
; FILE REFERENCE: 31.US3.CIP
; CURRENT APPLICATION NUMBER: US/09/663,600A
; CURRENT FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: 09/191,997
; PRIOR FILING DATE: 1998-11-13
; PRIOR APPLICATION NUMBER: 60/066,677
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/069,957
; PRIOR FILING DATE: 1997-12-17
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; PRIOR FILING DATE: 1998-08-10
; PRIOR APPLICATION NUMBER: 60/099,273
; PRIOR FILING DATE: 1998-09-04
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; LENGTH: 848
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 32..73
; OTHER INFORMATION: Von Heijne matrix
US-09-663-600A-27

Alignment Scores:
Pred. No.: 7.81e-129 Length: 848
Score: 1064.00 Matches: 208
Percent Similarity: 97.65% Conservative: 0
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US-09-989-724-387 (1-212) x US-09-663-600A-27 (1-848)

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QY 21 AlaGluAsnAlaPheLysValArgLeuSerIleArgThrAlaLeuGlyAspLysAlaTyr 40
Db 92 GCAGAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAGCATAT 151
QY 41 AlaTrpAspThrAsnGluGluTyrLeuPheLysAlaMetValAlaPheSerMetArgLys 60
Db 152 GCCTGGGATACCAATGAAGAAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAA 211
QY 61 ValProAsnArgGluAlaThrGluIleSerHisValLeuLeuCysAsnValThrGlnArg 80
Db 212 GTTCCCAACAGAGAGAACAGAAATTTCCCATGTCTCTTGTGCAATGTAAACCCAGAG 271

QY 81 ValSerPheTrpPheValValThrAspProSerLysAsnHisThrLeuProAlaValGlu 100
Db 272 GTATCATTCCTGGTTTGGTTACAGACCCCTTCAAAAAATCACACCCCTCTCTGTGTGAG 331
QY 101 ValGlnSerAlaIleArgMetAsnLysAsnArgIleAsnAsnAlaPhePheLeuAsnAsp 120
Db 332 GTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTCTAAATGAC 391
QY 121 GlnThrLeuGluPheLeuLysIleProSerThrLeuAlaProMetAspProSerVal 140
Db 392 CAAACTCTGGAATTTTAAAAATCCCTTCCACACTGCACCACCCATGGACCATCTGTG 451
QY 141 ProIleTrpIleIleIlePheGlyValIlePheCysIleIleIleValAlaIleAlaLeu 160
Db 452 CCCATCTGGATTATTATTATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTA 511
QY 161 LeuIleLeuSerGlyIleTrpGlnArgArgArgLysAsnLysGluProSerGluValAsp 180
Db 512 CTGATTTTATCAGGGATCTGGCAACGTADAARAAGAACAAGAACCATCTGAAGTGGAT 571
QY 181 AspAlaGluAspLysCysGluAsnMetIleThrIleGluAsnGlyIleProSerAspPro 200
Db 572 GACGCTGAARATAAATGTGAAACATGATCACAATTTGAAAATGGCATCCCTCTGATCCC 631
QY 201 LeuAspMetLysGly-GlyIleLeuMetMetProSer 212
Db 632 CTGACATGAAGGAGGCATATTAAATGATGCCTTCA 668

RESULT 4
US-09-621-976-5
; Sequence 5, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 5
; LENGTH: 848
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 32..697
; NAME/KEY: sig_peptide
; LOCATION: 32..73
; OTHER INFORMATION: Von Heijne matrix
US-09-621-976-5

Alignment Scores:
Pred. No.: 7.81e-129 Length: 848
Score: 1064.00 Matches: 208
Percent Similarity: 97.65% Conservative: 0
Best Local Similarity: 97.65% Mismatches: 4
Query Match: 96.55% Indels: 1
DB: 4 Gaps: 0

US-09-989-724-387 (1-212) x US-09-621-976-5 (1-848)

QY 1 MetLeuTrpLeuPhePheLeuValThrAlaIleHisAlaGluLeuCysGlnProGly 20
Db 32 ATGTTGGTCTCTCTTTTCTGGTACTGCTCATTCATGCTGAACCTCTGTCAACCCAGGT 91
QY 21 AlaGluAsnAlaPheLysValArgLeuSerIleArgThrAlaLeuGlyAspLysAlaTyr 40
Db 92 GCAGAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAGCATAT 151

; FILE REFERENCE: PF557
; CURRENT APPLICATION NUMBER: US/10/158,847
; CURRENT FILING DATE: 2002-06-03
; PRIOR APPLICATION NUMBER: 60/295,004
; PRIOR FILING DATE: 2001-06-04
; NUMBER OF SEQ ID NOS: 158
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 141
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-158-847-141

Alignment Scores:
Pred. No.: 2.21e-38 Length: 3396
Score: 376.00 Matches: 79
Percent Similarity: 67.27% Conservative: 32
Best Local Similarity: 47.88% Mismatches: 48
Query Match: 34.12% Indels: 6
DB: 4 Gaps: 3

US-09-989-724-387 (1-212) x US-10-158-847-141 (1-3396)

```
Qy 19 ProGlyAlaGluAsnAlaPheLysValArgLeuSerIleArgThrAlaLeuGlyAspLys 38
Db 1915 CCATATGCAGACCAAGCATCAAGTGAGGATAAGCCTAAAATCAGCTCTTGGAGATAAA 1974

Qy 39 AlaTyrAlaTrpAspThrAsnGluGluTyrLeuPheLysAlaMetValAlaPheSerMet 58
Db 1975 GCATATGAATGGAACGACCAATGAAATGTACCTGTTCGGATCATCTGTTGCATATGCTATG 2034

Qy 59 Arg-----LysValProAsnArgGluAlaThr---GluIleSerHisValLeu 73
Db 2035 AGGCAGTACTTTTAAAGTAAATAATCAGATGATTCCTTTTGGGAGGAGGATGTGCGA 2094

Qy 74 LeuCysAsnValThrGlnArgValSerPheTrpPheValValThrAspProSerLys--- 92
Db 2095 GTGGCTAATTGAAACCAAGAAATCTCCTTAATTTCTTTGTCACCTGCACCTAAAATGTG 2154

Qy 93 AsnHisThrLeuProAlaValGluValGlnSerAlaIleArgMetAsnLysAsnArgIle 112
Db 2155 TCTGATATCATCTCTAGAACTGAAGTTGAAAAGGCCATCAGGATGTCCCGGAGCGGTATC 2214

Qy 113 AsnAsnAlaPhePheLeuAsnAspGlnThrLeuGluPheLeuLysIleProSerThrLeu 132
Db 2215 AATGATGCTTCCGTCGTGAATGACAACAGCCTAGAGTTTCTGGGATACAGCCAACACTT 2274

Qy 133 AlaProMetAspProSerValProIleTrpIleIlePheGlyValIlePheCys 152
Db 2275 GGACCTCTTAACACGCCCCCTGTTCCATATGGCTGATTTTGGAGTTGTGATGGGA 2334

Qy 153 IleIleIleValAlaIleAlaLeuLeuIleLeuSerGlyIleTrpGlnArgArgLys 172
Db 2335 GTGATAGTGGTGGCATTGTCTCATCTTCTCACTGGGATCAGAGATCGAAGAGAAA 2394

Qy 173 AsnLysGluProSer 177
Db 2395 AATAAGCAAGAAGT 2409
```

RESULT 9

US-09-407-427-1
; Sequence 1, Application US/09407427
; Patent No. 6610497
; GENERAL INFORMATION:
; APPLICANT: Acton, Susan L.
; APPLICANT: Robison, Keith E.
; TITLE OF INVENTION: ANGIOTENSIN CONVERTING ENZYME HOMOLOG AND THERAPEUTIC
; TITLE OF INVENTION: AND DIAGNOSTIC USES THEREFOR
; FILE REFERENCE: MNI-132CP2
; CURRENT APPLICATION NUMBER: US/09/407,427
; CURRENT FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 09/163,648
; PRIOR FILING DATE: 1998-09-30

; PRIOR APPLICATION NUMBER: 08/989,299
; PRIOR FILING DATE: 1997-12-11
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 3396
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (82)..(2496)
US-09-407-427-1

Alignment Scores:
Pred. No.: 2.21e-38 Length: 3396
Score: 376.00 Matches: 79
Percent Similarity: 67.27% Conservative: 32
Best Local Similarity: 47.88% Mismatches: 48
Query Match: 34.12% Indels: 6
DB: 4 Gaps: 3

US-09-989-724-387 (1-212) x US-09-407-427-1 (1-3396)

```
Qy 19 ProGlyAlaGluAsnAlaPheLysValArgLeuSerIleArgThrAlaLeuGlyAspLys 38
Db 1915 CCATATGCAGACCAAGCATCAAGTGAGGATAAGCCTAAAATCAGCTCTTGGAGATAAA 1974

Qy 39 AlaTyrAlaTrpAspThrAsnGluGluTyrLeuPheLysAlaMetValAlaPheSerMet 58
Db 1975 GCATATGAATGGAACGACCAATGAAATGTACCTGTTCGGATCATCTGTTGCATATGCTATG 2034

Qy 59 Arg-----LysValProAsnArgGluAlaThr---GluIleSerHisValLeu 73
Db 2035 AGGCAGTACTTTTAAAGTAAATAATCAGATGATTCCTTTTGGGAGGAGGATGTGCGA 2094

Qy 74 LeuCysAsnValThrGlnArgValSerPheTrpPheValValThrAspProSerLys--- 92
Db 2095 GTGGCTAATTGAAACCAAGAAATCTCCTTAATTTCTTTGTCACCTGCACCTAAAATGTG 2154

Qy 93 AsnHisThrLeuProAlaValGluValGlnSerAlaIleArgMetAsnLysAsnArgIle 112
Db 2155 TCTGATATCATCTCTAGAACTGAAGTTGAAAAGGCCATCAGGATGTCCCGGAGCGGTATC 2214

Qy 113 AsnAsnAlaPhePheLeuAsnAspGlnThrLeuGluPheLeuLysIleProSerThrLeu 132
Db 2215 AATGATGCTTCCGTCGTGAATGACAACAGCCTAGAGTTTCTGGGATACAGCCAACACTT 2274

Qy 133 AlaProMetAspProSerValProIleTrpIleIlePheGlyValIlePheCys 152
Db 2275 GGACCTCTTAACACGCCCCCTGTTCCATATGGCTGATTTTGGAGTTGTGATGGGA 2334

Qy 153 IleIleIleValAlaIleAlaLeuLeuIleLeuSerGlyIleTrpGlnArgArgLys 172
Db 2335 GTGATAGTGGTGGCATTGTCTCATCTTCTCACTGGGATCAGAGATCGAAGAGAAA 2394

Qy 173 AsnLysGluProSer 177
Db 2395 AATAAGCAAGAAGT 2409
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RESULT 10

US-10-158-847-137
; Sequence 137, Application US/10158847
; Patent No. 6592865
; GENERAL INFORMATION:
; APPLICANT: Tom Parry et al.
; TITLE OF INVENTION: Method and Compositions for Modulating ACE-2 Activity
; FILE REFERENCE: PF557
; CURRENT APPLICATION NUMBER: US/10/158,847
; CURRENT FILING DATE: 2002-06-03
; PRIOR APPLICATION NUMBER: 60/295,004
; PRIOR FILING DATE: 2001-06-04
; NUMBER OF SEQ ID NOS: 158
; SOFTWARE: PatentIn version 3.1

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; SEQ ID NO 137
; LENGTH: 2920
; TYPE: DNA
; ORGANISM: homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1707)..(1707)
; OTHER INFORMATION: n equals any amino acid
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (2702)..(2702)
; OTHER INFORMATION: n equals any amino acid
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (2749)..(2749)
; OTHER INFORMATION: n equals any amino acid
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (2757)..(2757)
; OTHER INFORMATION: n equals any amino acid
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (2788)..(2789)
; OTHER INFORMATION: n equals any amino acid
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (2819)..(2819)
; OTHER INFORMATION: n equals any amino acid
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (2835)..(2835)
; OTHER INFORMATION: n equals any amino acid
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (2856)..(2856)
; OTHER INFORMATION: n equals any amino acid
; OTHER INFORMATION: n equals any amino acid
US-10-158-847-137
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Alignment Scores:
Pred. No.: 2.86e-36 Length: 2920
Score: 359.00 Matches: 75
Percent Similarity: 67.30% Conservative: 32
Best Local Similarity: 47.17% Mismatches: 46
Query Match: 32.58% Indels: 6
DB: 4 Gaps: 3
```

```
US-09-989-724-387 (1-212) x US-10-158-847-137 (1-2920)
QY 19 ProGlyAlaGluAsnAlaPheLysValArgLeuSerIleArgThrAlaLeuGlyAspLys 38
DB 1863 CCATATGCAGACCAAGCATCAAGTGAAGGATAAGCCTAAATCAGCTCTTGGAGATAAA 1922
QY 39 AlaTyrAlaTyrAspThrAsnGluGluTyrPheLysAlaMetValAlaPheSerMet 58
DB 1923 GCATATGAATGGAACGACAATGAATGTACCTGTTCCGATCATCTGTTGCATATGCTATG 1982
QY 59 Arg-----LysValProAsnArgGluAlaThr---GluIleSerHisValLeu 73
DB 1983 AGGCAGTACTTTTAAAGTAAAGTAAATCAGATGATCTTTTGGGAGGAGGATGTGCGA 2042
QY 74 LeuCysAsnValThrGlnArgValSerPheThrPheValValThrAspProSerLys--- 92
DB 2043 GTGGCTAATTGAAACCAAGATCTCTTTAATTTCTTTGTCACCTGCACCTAAATATGTG 2102
QY 93 AsnHisThrLeuProAlaValGluValGlnSerAlaIleArgMetAsnLysAsnArgIle 112
DB 2103 TCTGATATCATCTCTAGAACTGAAGTTGAAAGGCCATCAGGATGTCCCGAGCCGTATC 2162
QY 113 AsnAsnAlaPhePheLeuAsnAspGlnThrLeuGluPheLeuLysIleProSerThrLeu 132
DB 2163 AATGATGCTTTCGCTCTGAATGACGACAGCCTAGAGTTTCTGGGGATACAGCCAACACTT 2222
QY 133 AlaProProMetAspProSerValProIleThrIleIlePheGlyValIlePheCys 152
```

```
Db 2223 GGACCTCCTAACCCAGCCCCCTGTTTCCATATGGCTGATGTTTTTGGAGTTGTGATGGGA 2282
QY 153 IleIleIleValAlaIleAlaLeuLeuIleLeuSerGlyIleTrpGlnArgArgArg 171
Db 2283 GTGATAGTGGTGGCATTGTCTATCTGATCTTCACTGGGATCAGAGATCGGAAGAAG 2339
RESULT 11
US-09-289-349-6
; Sequence 6, Application US/09289349
; Patent No. 6277574
; GENERAL INFORMATION:
; APPLICANT: Walker, Michael, G.
; APPLICANT: Volkumth, Wayne
; APPLICANT: Klinger, Tod, M.
; APPLICANT: Azimzai, Yalda
; APPLICANT: Yue, Henry
; TITLE OF INVENTION: GENES ASSOCIATED WITH DISEASES OF THE KIDNEY
; FILE REFERENCE: PB-0010 US
; CURRENT APPLICATION NUMBER: US/09/289,349
; CURRENT FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PERL Program
; SEQ ID NO 6
; LENGTH: 862
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: 2580580CT1
US-09-289-349-6
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Alignment Scores:
Pred. No.: 6.21e-27 Length: 862
Score: 281.00 Matches: 57
Percent Similarity: 98.28% Conservative: 0
Best Local Similarity: 98.28% Mismatches: 0
Query Match: 25.50% Indels: 1
DB: 3 Gaps: 0
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US-09-989-724-387 (1-212) x US-09-289-349-6 (1-862)

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QY 156 ValAlaIleAlaLeuLeuIleLeuSerGlyIleTrpGlnArgArgArgLysAsnLysGlu 175
Db 1 GTTGCATTTGCACACTACTGATTTTATCAGGGATCTGGCAACGCTAGAGAAAGAACAAAGAA 60
QY 176 ProSerGluValAspAspAlaGluAspLysCysGluAsnMetIleThrIleGluAsnGly 195
Db 61 CCATCTGAAGTGGATGACGCTGAAGATAAGTGTGAAAAACATGATCACAATTTGAAATGGC 120
QY 196 IleProSerAspProLeuAspMetLysGly-GlyIleLeuMetMetProSer 212
Db 121 ATCCCTCTGATCCCTGGACATGAAGGGAGGCGCATATTAATGATGCCTTCA 172
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RESULT 12

```
US-09-280-116-40/c
; Sequence 40, Application US/09280116A
; Patent No. 6331427
; GENERAL INFORMATION:
; APPLICANT: Robison, Keith E.
; TITLE OF INVENTION: Nucleic Acid Molecules Encoding Human Protease Homologs
; FILE REFERENCE: 5800-24, 035800/176965
; CURRENT APPLICATION NUMBER: US/09/280,116A
; CURRENT FILING DATE: 1999-03-26
; NUMBER OF SEQ ID NOS: 268
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 40
; LENGTH: 2350
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: angiotensin-converting enzyme
US-09-280-116-40
```


REFERENCE/DOCKET NUMBER: 31340
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 41:
SEQUENCE CHARACTERISTICS:
LENGTH: 3136 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-188-228-41

Alignment Scores:
Pred. No.: 0.322 Length: 3136
Score: 90.00 Matches: 52
Percent Similarity: 35.39% Conservative: 34
Best Local Similarity: 21.40% Mismatches: 91
Query Match: 8.17% Indels: 66
DB: 1 Gaps: 11

US-09-989-724-387 (1-212) x US-08-188-228-41 (1-3136)

Qy 13 HisAlaGluLeuCysGlnProGlyAlaGluAsnAlaPheLysValArgLeuSerIleArg 32
Db 1835 CACACTGACTTGGAGACAGATTCAACATCATATGCAGATGATGGGAAGATAACACTGGCG 1894

Qy 33 ThrAlaLeuGlyAspLysAlaTyrAlaTrpAspThr----- 44
Db 1895 ACCCCACTGGACAGAGAACTAAGTGTGGCAACATCTCCATCATTTGCTACTGATGATC 1954

Qy 45 ---AsnGluGluTyrLeuPheLysAlaMetValAlaPheSerMetArgLysValProAsn 63
Db 1955 AGGAACACACAGTCAGATATCGCGAGTGCCTGTGCTATTAAAGTGTGATGTC---AAT 2011

Qy 64 ArgGluAlaThrGluIleSer-----HisValLeuLeuCys----- 75
Db 2012 GACAAAGCCCTGAAATTCGCGTCCGAATATGAGGCATTTTATGTGAAATGGAACCC 2071

Qy 76 ---AsnValThrGlnArgValSerPheTrpPheValValThrAspProSerLysAsnHis 94
Db 2072 GGCCAAGTCATTCAAAACAGTAAGCGCC---ATGGACAAAGACGATCCCAAAATGACAT 2128

Qy 95 -----ThrLeuProAlaValGluValGlnSerAlaIleArgMetAsnLys 109
Db 2129 TTTTCTTGTACAGTCTTCTCCAGAAATGGTCAACAAACCCAAATTTCCATCAAGAA 2188

Qy 110 AsnArgIleAsnAsnAlaPhePheLeu-----AsnAspGlnThrLeu 123
Db 2189 AACGAAGATAATTCCTGAGCATTTCTGGCAAAACATAATGATTCAACCGCCAGAGCAA 2248

Qy 124 GluPheLeuLysIleProSerThrLeuAla-----ProMetMetAspProSer 139
Db 2249 GAAGTCTACCTTCTGCTATCGTATCAGTGACAGTGGGAACCCCTCTGAGTAGCACC 2308

Qy 140 ValProIleTrpIleIleIlePheGly----- 148
Db 2309 AGTACCCTGACCATCCGCTCTGTGGCTGTAGCAATGACGGGTGTTGCTGCTGCAAT 2368

Qy 149 -----ValIlePhe 151
Db 2369 GTCGAAGCTTATGCTCTTCTTATTTGGGCTCAGTATGGGCGGTAAATGCTATATAGCC 2428

Qy 152 CysIleIleIleValAlaIleAlaLeuLeuIleLeuSerGlyIleTrpGlnArgArg 171
Db 2429 TGCATCATTTTGTCTGCTGCTCATTTGTGTTCTGTTTC-----GTTACCTGAGGGCGCAT 2482

Qy 172 LysAsnLysGluProSerGluValAspAlaGluAspLysCysGluAsnMetIleThr 191
Db 2483 AAAAAAT---GAACCACTAATAATCAAGATGATGAAGCGTTTCGAGAAACATCATTCGC 2539

Qy 192 IleGluAsn 194

Db 2540 TACGACGAC 2548
RESULT 15
US-08-332-638-41
Sequence 41, Application US/08332638
Patent No. 5646250
GENERAL INFORMATION:
APPLICANT: Suzuki, Shintaro
TITLE OF INVENTION: CADHERIN MATERIALS AND METHODS
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
ADDRESSEE: Borun
STREET: 6300 Sears Tower, 233 S. Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/332,638
FILING DATE: 01-NOV-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/872,643
FILING DATE: 17 APR 1992
APPLICATION NUMBER: US/08/049,460
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: No. 5646250and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31340
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 41:
SEQUENCE CHARACTERISTICS:
LENGTH: 3136 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-332-638-41

Alignment Scores:
Pred. No.: 0.322 Length: 3136
Score: 90.00 Matches: 52
Percent Similarity: 35.39% Conservative: 34
Best Local Similarity: 21.40% Mismatches: 91
Query Match: 8.17% Indels: 66
DB: 1 Gaps: 11

US-09-989-724-387 (1-212) x US-08-332-638-41 (1-3136)

Qy 13 HisAlaGluLeuCysGlnProGlyAlaGluAsnAlaPheLysValArgLeuSerIleArg 32
Db 1835 CACACTGACTTGGAGACAGATTCAACATCATATGCAGATGATGGGAAGATAACACTGGCG 1894

Qy 33 ThrAlaLeuGlyAspLysAlaTyrAlaTrpAspThr----- 44
Db 1895 ACCCCACTGGACAGAGAACTAAGTGTGGCAACATCTCCATCATTTGCTACTGATGATC 1954

Qy 45 ---AsnGluGluTyrLeuPheLysAlaMetValAlaPheSerMetArgLysValProAsn 63
Db 1955 AGGAACACACAGTCAGATATCGCGAGTGCCTGTGCTATTAAAGTGTGATGTC---AAT 2011

Qy 64 ArgGluAlaThrGluIleSer-----HisValLeuLeuCys----- 75

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Db      2012 GACAAACGCCCCCTGAATTCGCGTCCGAATATGAGGCATTTTATGTGAAATGGAAAAACC 2071
QY      76 ---AsnValThrGlnArgValSerPheTrpPheValValThrAspProSerLysAsnHis 94
Db      2072 GGCCAAAGTCATTCAAACAGTAAGCGC---ATGGACAAAGACGATCCCAAAAAATGGACAT 2128
QY      95 -----ThrLeuProAlaValGluValGlnSerAlaIleArgMetAsnLys 109
Db      2129 TTTTCTGTACAGTCTTCTTCAGAAATGGTCAACACCCAAATTTTACCACATCAAGAAA 2188
QY      110 AsnArgIleAsnAsnAlaPhePheLeu-----AsnAspGlnThrLeu 123
Db      2189 AACGAAGATAAATCCCTGAGCATTCCTGGCAAAACATAATGGATTCAACCGCCAGAAAGCAA 2248
QY      124 GluPheLeuLysIleProSerThrLeuAla-----ProMetMetAspProSer 139
Db      2249 GAAGTCTACCTTCTGCTGCTATCGTGATCAGTGACAGTGGGAACCCCTCTGAGTAGCACC 2308
QY      140 ValProIleTrpIleIleIlePheGly-----ValIlePhe 151
Db      2309 AGTACCCGTGACCATCCGCGTCTGTGGCTGTAGCAATGACGGCGTGGTTCAAGTCGTGCAAT 2368
QY      149 -----ValIlePhe 151
Db      2369 GTCGAAGCTTATGTCCTTCCTATTGGGCTCAGTANGGCGCGTTAATTGCTATATTAGCC 2428
QY      152 CysIleIleIleValAlaIleAlaLeuLeuIleLeuSerGlyIleTrpGlnArgArg 171
Db      2429 TGCATCATTTTGTGCTGCTCATTTGTGTTCTGTTT-----GTTACCCCTGAGGCGGCAT 2482
QY      172 LysAsnLysGluProSerGluValAlaAspAlaGluAspLysCysGluAsnMetIleThr 191
Db      2483 AAAAAAT---GAACCACTAATAATCAAGATGATGAAGACGTTTCGAGAAAAACATCATTCGC 2539
QY      192 IleGluAsn 194
Db      2540 TAGGACGAC 2548
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Job time : 238 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: April 4, 2004, 03:17:39 ; Search time 411 Seconds
(without alignments)
1929.247 Million cell updates/sec

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2466186 seqs, 1870095128 residues

Total number of hits satisfying chosen parameters: 4932372

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-LOOPEXT=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0
-MAXLEN=2000000000 -USER=US09989724 @CGN 1 1 57 @runat_31032004_081143_13358
-NCPU=6 -ICPU=3 -NO MAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100
-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
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Database : Published Applications NA:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
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ALIGNMENTS

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US-09-989-722-386
; Sequence 386, Application US/09989722
; Patent No. US20020072067A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Baton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.

APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730P1C63
CURRENT APPLICATION NUMBER: US/09/989,722
CURRENT FILING DATE: 2001-11-19
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
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; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Alignment Scores:

Pred. No.: 3,65e-147 Length: 1346
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Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
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US-09-989-724-387 (1-212) x US-09-989-722-386 (1-1346)

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RESULT 2

US-09-989-723-386
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; Patent No. US20020072092A1
; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Baton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Pong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same

; FILE REFERENCES: P2730P1C62

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3.65e-147

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1346

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Query Match: 100.00% Indels: 0
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US-09-989-724-387 (1-212) x US-09-989-723-386 (1-1346)

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Db 127 GCCTGGGATACCAATGAAGATACCTCTTCAAGCGATGGTAGCTTCTCCATGAGAAA 186
QY 61 ValProAsnArgGluAlaThrGluIleSerHisValLeuLeuCysAsnValThrGlnArg 80
Db 187 GTTCCCAACAGAGAACCAACGAAATTTCCCATGTCTTCTGCAATGTAAACCCAGG 246
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Db 247 GTATCATTTCTGGTTGTGGTTACAGACCTTCAAAAAATCACACCTTCTCTGCTGTGAG 306
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Db 307 GTGCAATCAGCATAGAATGAACAAAGAACCGGATCAACATGCTCTTCTTAAATGAC 366
QY 121 GlnThrLeuGluPheLeuLysIleProSerThrLeuAlaProProMetAspProSerVal 140
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QY 141 ProIleTrpIleIleIlePheGlyValIlePheCysIleIleValAlaIleAlaLeu 160
Db 427 CCCATCTGGATTATTATTGTTGTGATATTTTGCATCATCATAGTTGCAATGCACTA 486
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Db 487 CTGATTTTATCAGGGATCTGGCAACGTAGAACAAAGAACCAACCATCTGAAGTGGAT 546
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QY 201 LeuAspMetLysGlyGlyIleLeuMetMetProSer 212
Db 607 CTGGACATGAAGGGGGGCATATTAAATGATGCCTTCA 642

RESULT 3

US-09-989-279-386
; Sequence 386, Application US/09989279
; Patent No. US20020072496A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James

; APPLICANT: Paoni, Nicholas P.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730PIC56
; CURRENT APPLICATION NUMBER: US/09/989,279
; CURRENT FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
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; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

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Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-09-989-724-387 (1-212) x US-09-989-279-386 (1-1346)

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Qy 21 AlaGluAsnAlaPheLysValArgLeuSerIleArgThrAlaLeuGlyAspLysAlaTyr 40
Db 67 GCAGAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 126
Qy 41 AlaTrpAspThrAsnGluGluTyrLeuPheLysAlaMetValAlaPheSerMetArgLys 60
Db 127 GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA 186
Qy 61 ValProAsnArgGluAlaThrGluIleSerHisValLeuLeuCysAsnValThrGlnArg 80
Db 187 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCTACTTTGCAATGTAAACCCAGAG 246
Qy 81 ValSerPheTrrPheValValThrAspProSerLysAsnHisThrLeuProAlaValGlu 100
Db 247 GTATCATTTCTGGTTGTGGTTACAGACCCCTTCAAAAATACACACCCCTCTCTGTGTGAG 306
Qy 101 ValGlnSerAlaIleArgMetAsnLysAsnArgIleAsnAsnAlaPhePheLeuAsnAsp 120
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Qy 121 GlnThrLeuGluPheLeuLysIleProSerThrLeuAlaProProMetAspProSerVal 140
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/ PRIOR FILING DATE: 1998-07-07
/ PRIOR APPLICATION NUMBER: 60/092182
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Pred. No.: 3.65e-147 Length: 1346
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Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-09-989-724-387 (1-212) x US-09-989-727-386 (1-1346)

Qy 1 MetLeuTrpLeuLeuPhePheLeuValThrAlaIleHisAlaGluLeuCysGlnProGly 20
Db 7 ATGTTGGGCTGCTCTTTTCTGGTGACTGCCATTCACTGCTGAACCTCTCTCAACCCAGGT 66
Qy 21 AlaGluAsnAlaPheLysValArgLeuSerIleArgThrAlaLeuGlyAspLysAlaTyr 40
Db 67 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 126
Qy 41 AlaTrpAspThrAsnGluGluTyrluPheLysAlaMetValAlaPheSerMetArgLys 60
Db 127 GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGGATGGTAGCTTTCTCCATGAGAAAA 186
Qy 61 ValProAsnArgGluAlaThrGluIleSerHisValLeuLeuCysAsnValThrGlnArg 80
Db 187 GTTCCCAACAGAGAGCAACAGAAATTTCCCATGTCTTACTTTGCAATGTAAACCCAGAG 246
Qy 81 ValSerPheTrpPheValValThrAspProSerLysAsnHisThrLeuProAlaValGlu 100
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Qy 121 GlnThrLeuGluPheLeuLysIleProSerThrLeuAlaProProMetAspProSerVal 140
Db 367 CAAACTCTGGAAATTTTAAAAATCCCTTCCACACTTGACACCCATGGACCCATCTGTG 426
Qy 141 ProIleTrpIleIleIlePheGlyValIlePheCysIleIleIleValAlaIleAlaLeu 160
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Qy 181 AspAlaGluAspLysCysGluAsnMetIleThrIleGluAsnGlyIleProSerAspPro 200
Db 547 GACGCTGAAGATAAGTGTGAAAAACATGATCACAATGAAAATGGCATCCCTCTGATCCC 606
Qy 201 LeuAspMetLysGlyIleLeuMetMetProSer 212
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RESULT 5

US-09-989-731-386
; Sequence 386, Application US/09989731
; Patent No. US20020103125A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
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; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C70
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; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Alignment Scores:

Pred. No.:	3.65e-147	Length:	1346
Score:	1102.00	Matches:	212
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	9	Gaps:	0

US-09-989-724-387 (1-212) x US-09-989-731-386 (1-1346)

Qy	1	MetLeuTrpLeuPheLeuValThrAlaIleHisAlaGluLeuCysGlnProGly	20
Db	7	ATGTTGGCTGCTCTTTTCTGGTGACTGCCATTCAGCTGAACCTGTGCAACCAAGT	66
Qy	21	AlaGluAsnAlaPheLysValArgLeuSerIleArgThrAlaLeuGlyAspLysAlaTyr	40
Db	67	GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT	126
Qy	41	AlaTrpAspThrAsnGluGluTyrLeuPheLysAlaMetValAlaPheSerMetArgLys	60
Db	127	GCCTGGGATACCAATGAAGATACCTCTCAAGCGATGGTAGCTTTCTCCATGAGAAA	186
Qy	61	ValProAsnArgGluAlaThrGluIleSerHisValLeuLeuCysAsnValThrGlnArg	80
Db	187	GTTCCCAACAGAGAGAACAGAAATTTCCCATGTCTTCTTCCATGTAACCCAGAGG	246
Qy	81	ValSerPheTrpPheValThrAspProSerLysAsnHisThrLeuProAlaValGlu	100
Db	247	GTATCATCTCTGGTTTGGTTTACAGACCTTCAAAAAATCACACCTTCTCTGCTGTGAG	306
Qy	101	ValGlnSerAlaIleArgMetAsnLysAsnArgIleAsnAsnAlaPhePheLeuAsnAsp	120
Db	307	GTGCAATCAGCCCATAGAATGAACAGACCGGATCAACAATGCCTTTCTTTCTAAATGAC	366

Qy	121	GlnThrLeuGluPheLeuLysIleProSerThrLeuAlaProProMetAspProSerVal	140
Db	367	CAAACTCTGGAATTTTAAAAAATCCCTTCCACACTTGCACACCCCATGGACCATCTGTG	426
Qy	141	ProIleTrpIleIlePheGlyValIlePheCysIleIleIleValAlaIleAlaLeu	160
Db	427	CCCATCTGGATTATTATATTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTA	486
Qy	161	LeuIleLeuSerGlyIleTrpGlnArgArgLysAsnLysGluProSerGluValAsp	180
Db	487	CTGATTTTATCAGGGATCTGGCAACGCTAGAAGAAAGAACAAAGAACCATCTGGAAGTGGAT	546
Qy	181	AspAlaGluAspLysCysGluAsnMetIleThrIleGluAsnGlyIleProSerAspPro	200
Db	547	GACGCTGAAGATAAGTGTGAAAAACATGATCACAATTTGAAAATGGCATCCCCCTCTGATCCC	606
Qy	201	LeuAspMetLysGlyGlyIleLeuMetMetProSer	212
Db	607	CTGGACATGAAGGGGGCATATTATATGATGCCTTCA	642

RESULT 6

US-09-989-732-386
; Sequence 386, Application US/09989732
; Patent No. US20020123463A1

GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C57
; CURRENT APPLICATION NUMBER: US/09/989,732
; CURRENT FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066770
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/075945
; PRIOR FILING DATE: 1998-02-25
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/083322
; PRIOR FILING DATE: 1998-04-28
; PRIOR APPLICATION NUMBER: 60/084600
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/087106

; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Alignment Scores:

Pred. No.:	3.65e-147	Length:	1346
Score:	1102.00	Matches:	212
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	9	Gaps:	0

US-09-989-724-387 (1-212) x US-09-989-732-386 (1-1346)

Qy	1	MetLeuTrpLeuLeuPhePheLeuValThrAlaIleHisAlaGluLeuCysGlnProGly	20
Db	7	ATGTTGGCTGCTCTTTTCTGGTGACTGCCATTTCATGCTGAACCTCTGTCAACCCAGGT	66
Qy	21	AlaGluAsnAlaPheLysValArgLeuSerIleArgThrAlaLeuGlyAspLysAlaTyr	40
Db	67	GCAGAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT	126
Qy	41	AlaTrpAspThrAsnGluGluTyrLeuPheLysAlaMetValAlaPheSerMetArgLys	60
Db	127	GCCTGGGATACCAATGAAGATACCTTCAAAAGCGATGGTAGCTTTCTCCATGAGAAA	186
Qy	61	ValProAsnArgGluAlaThrGluIleSerHisValLeuLeuCysAsnValThrGlnArg	80
Db	187	GTTCCCAACAGAGAGCAACAGAAATTTCCCATGTCTTACTTTGCAATGTAACCCAGAG	246
Qy	81	ValSerPheTrpPheValValThrAspProSerLysAsnHisThrLeuProAlaValGlu	100
Db	247	GTATCAATCTGTTTGGTTGTACAGACCTTCAAAATACACACCTTCTGCTGTGGAG	306
Qy	101	ValGlnSerAlaIleArgMetAsnLysAsnArgIleAsnAsnAlaPhePheLeuAsnAsp	120
Db	307	GTGCAATCAGCCATAGATGAACAGACCGGATCAACAATGCCCTTCTTCTTAAATGAC	366
Qy	121	GlnThrLeuGluPheLeuLysIleProSerThrLeuAlaProProMetAspProSerVal	140
Db	367	CAAACTCTGGAATTTTAAAAATCCCTTCCACACTTGCACCACTGACCCCATCTGTG	426
Qy	141	ProIleTrpIleIlePheGlyValIlePheCysIleIleValAlaIleAlaLeu	160
Db	427	CCCATCTGGATTATTATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCAC	486
Qy	161	LeuIleLeuSerGlyIleTrpGlnArgArgLysAsnLysGluProSerGluValAsp	180
Db	487	CTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAAGTGG	546
Qy	181	AspAlaGluAspLysCysGluAsnMetIleThrIleGluAsnGlyIleProSerAspPro	200
Db	547	GACGCTGAAGATAGTGTGAAACATGATCACAATTGAAAATGGCATCCCTCTGTATCC	606
Qy	201	LeuAspMetLysGlyGlyIleLeuMetMetProSer	212
Db	607	CTGGACATGAAGGGGGCATATTATATGATGCTTCA	642

RESULT 7

US-09-991-073-386
; Sequence 386, Application US/09991073
; Patent No. US2002127576A1

GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
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; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C15
; CURRENT APPLICATION NUMBER: US/09/991,073
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
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; PRIOR APPLICATION NUMBER: 60/091360
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; PRIOR APPLICATION NUMBER: 60/091478
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091544
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/091519
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091626
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091633
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Alignment Scores:

Pred. No.: 3.65e-147 Length: 1346
Score: 1102.00 Matches: 212
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-09-989-724-387 (1-212) x US-09-991-073-386 (1-1346)

Qy 1 MetLeuTrpLeuLeuPhePheLeuValThrAlaIleHisAlaGluLeuCysGlnProGly 20
Db 7 ATGTTGGGCTGCTCTTTTCTGGTGAAGTCCATTCATGCTGAACCTCTGCAACCAGGT 66
Qy 21 AlaGluAsnAlaPheLysValArgLeuSerIleArgThrAlaLeuGlyAspLysAlaTyr 40
Db 67 GCAGAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAGCATAT 126
Qy 41 AlaTrpAspThrAsnGluGluTyrLeuPheLysAlaMetValAlaPheSerMetArgLys 60
Db 127 GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA 186
Qy 61 ValProAsnArgGluAlaThrGluIleSerHisValLeuLeuCysAsnValThrGlnArg 80
Db 187 GTTCCCAACAGAGAGCAACAGAAATTTCCCATGTCTTACTTTTGCATGTAAACCCAGAG 246
Qy 81 ValSerPheTrpPheValValThrAspProSerLysAsnHisThrLeuProAlaValGlu 100
Db 247 GTATCATTCGTGGTTGGTTACAGACCCCTTCAAAAAAATCACACCCCTTCTGCTGTGAG 306
Qy 101 ValGlnSerAlaIleArgMetAsnLysAsnArgIleAsnAsnAlaPhePheLeuAsnAsp 120

Db 307 GTGCAATCAGCCATAAGAAATGAACAAGAACCGGATCAACAATGCCTTCTTCTAAATGAC 366
Qy 121 GlnThrLeuGluPheLeuLysIleProSerThrLeuAlaProProMetAspProSerVal 140
Db 367 CAAACTCTGGAATTTTAAATAATCCCTTCCACACTTGCCACCAACCCATGGACCCATCTGTG 426
Qy 141 ProIleTrpIleIleIlePheGlyValIlePheCysIleIleIleValAlaIleAlaLeu 160
Db 427 CCCATCTGGATTATTATATTGGTGGATTTTGCATCATCATAGTTGCAATTGCACTA 486
Qy 161 LeuIleLeuSerGlyIleTrpGlnArgArgArgLysAsnLysGluProSerGluValAsp 180
Db 487 CTGATTTTATCAGGATCTGGCAACGCTAGAGAAGAAACAACCAACCATCTGAAGTGGAT 546
Qy 181 AspAlaGluAspLysCysGluAsnMetIleThrIleGluAsnGlyIleProSerAspPro 200
Db 547 GACGCTGAAGATAAGTGTGAAAAACATGATCACAATTGAAATGGCATCCCTCTGTATCCC 606
Qy 201 LeuAspMetLysGlyGlyIleLeuMetMetProSer 212
Db 607 CTGGACATGAAGGGGGGCATATTATATGATGCCTTCA 642

RESULT 8

US-09-990-442-386
; Sequence 386, Application US/09990442
; Patent No. US20020132252A1

GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary B.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

; TITLE OF INVENTION: Acids Encoding the Same

; FILE REFERENCE: P2730P1C8

; CURRENT APPLICATION NUMBER: US/09/990,442

; CURRENT FILING DATE: 2001-11-14

; PRIOR APPLICATION NUMBER: 60/049787

; PRIOR FILING DATE: 1997-06-16

; PRIOR APPLICATION NUMBER: 60/062250

; PRIOR FILING DATE: 1997-10-17

; PRIOR APPLICATION NUMBER: 60/065186

; PRIOR FILING DATE: 1997-11-12

; PRIOR APPLICATION NUMBER: 60/065311

; PRIOR FILING DATE: 1997-11-13

; PRIOR APPLICATION NUMBER: 60/066770

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; PRIOR FILING DATE: 1998-03-20

; PRIOR APPLICATION NUMBER: 60/083322

; PRIOR FILING DATE: 1998-04-28

; PRIOR APPLICATION NUMBER: 60/084600

; PRIOR FILING DATE: 1998-05-07

; PRIOR APPLICATION NUMBER: 60/087106

; PRIOR FILING DATE: 1998-05-28

; PRIOR APPLICATION NUMBER: 60/087607

; PRIOR FILING DATE: 1998-06-02

; PRIOR APPLICATION NUMBER: 60/087609

; PRIOR FILING DATE: 1998-06-02

; PRIOR APPLICATION NUMBER: 60/087759

; PRIOR FILING DATE: 1998-06-02

; PRIOR APPLICATION NUMBER: 60/087827

; PRIOR FILING DATE: 1998-06-03

; PRIOR APPLICATION NUMBER: 60/088021

; PRIOR FILING DATE: 1998-06-04

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; PRIOR FILING DATE: 1998-07-02
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; PRIOR FILING DATE: 1998-07-02
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; PRIOR FILING DATE: 1998-07-02

; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Alignment Scores:

Pred. No.: 3.65e-147 Length: 1346
Score: 1102.00 Matches: 212
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-09-989-724-387 (1-212) x US-09-990-442-386 (1-1346)

Qy 1 MetLeuTrpLeuLeuPhePheLeuValThrAlaIleHisAlaGluLeuCysGlnProGly 20
Db 7 ATGTTGTGGCTGCTCTTTTTCTGGTGACTGCCATTTCATGCTGAACCTCTCTCAACCCAGGT 66
Qy 21 AlaGluAsnAlaPheLysValArgLeuSerIleArgThrAlaLeuGlyAspLysAlaTyr 40
Db 67 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 126
Qy 41 AlaTrpAspThrAsnGluGluTyrLeuPheLysAlaMetValAlaPheSerMetArgLys 60
Db 127 GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTTCCCATGAGAAAA 186
Qy 61 ValProAsnArgGluAlaThrGluIleSerHisValLeuLeuCysAsnValThrGlnArg 80
Db 187 GTTCCCAACAGAGAGAACCAACAGAAATTTCCCATGTCTTCTTCAATGTAAACCCAGAG 246
Qy 81 ValSerPheTrpPheValValThrAspProSerLysAsnHisThrLeuProAlaValGlu 100
Db 247 GTATCATCTGGTTTGTGGTTACAGACCCCTTCAAAGAAATGCAATGCCTTCTCTGTGTGAG 306
Qy 101 ValGlnSerAlaIleArgMetAsnLysAsnArgIleAsnAsnAlaPhePheLeuAsnAsp 120
Db 307 GTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAAATGCCTTCTTCTTAAATGAC 366
Qy 121 GlnThrLeuGluPheLeuLysIleProSerThrLeuAlaProProMetAspProSerVal 140
Db 367 CAAACTCTGGAATTTTAAATAATCCCTTCCACACTTGCACCCACCCCATGGACCCCATCTGTG 426
Qy 141 ProIleTrpIleIleIlePheGlyValIlePheCysIleIleIleValAlaIleAlaLeu 160
Db 427 CCCATCTGGATTATATATATTTGGTGTGATATTTTGGCATCATCATAGTTGCAATTGCACTA 486
Qy 161 LeuIleLeuSerGlyIleTrpGlnArgArgArgLysAsnLysGluProSerGluValAsp 180
Db 487 CTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAAAGAACCAATCTGGAAGTGGAT 546
Qy 181 AspAlaGluAspLysCysGluAsnMetIleThrIleGluAsnGlyIleProSerAspPro 200
Db 547 GACGCTGAAGATAGTGTGAAAACATGATCACAATTTGAAAATGGCATCCCTCTGATCCC 606
Qy 201 LeuAspMetLysGlyGlyIleLeuMetMetProSer 212
Db 607 CTGGACATGAAGGGGGCATATTATATGATGCCTTCA 642

RESULT 9

US-09-991-163-386
; Sequence 386, Application US/09991163
; Patent No. US20020132253A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman

```

; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary B.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C17
; CURRENT APPLICATION NUMBER: US/09/991.163
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
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; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

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Pred. No.:	3,658-147	Length:	1346
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DB:	9	Gaps:	0

US-09-989-724-387 (1-212) x US-09-991-163-386 (1-1346)

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QY	21	AlaGluAsnAlaPheLysValArgLeuSerIleArgThrAlaLeuGlyAspLysAlaTyr	40
Db	67	GCAGAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGAGATAAAGCATAT	126
QY	41	AlaTrpAspThrAsnGluGluTyrLeuPheLysAlaMetValAlaPheSerMetArgLys	60
Db	127	GCTGGGATACCAATGAAGATACTCTTCAAAGCGATGGTAGTTTCTCCATGAGAAA	186
QY	61	ValProAsnArgGluAlaThrGluIleSerHisValLeuLeuCysAsnValThrGlnArg	80
Db	187	GTTCACCAACAGAGAACACAGAATTTCCCTACTTCTCAATGTAAACAGAG	246
QY	81	ValSerPheTrpPheValThrAspProSerLysAsnHisThrLeuProAlaValGlu	100

Db	247	GTATCATTTCTGGTTTGTGGTTACAGACCCCTTCAAAAAATCACACCCCTTCTGCTGTGAG	306
QY	101	ValGlnSerAlaIleArgMetAsnLysAsnArgIleAsnAlaPheLeuAsnAsp	120
Db	307	GTGCAATCAGCCATAGAATGAACAAGACCGGATCAACAATGCCTTCTTTCTAAATGAC	366
QY	121	GlnThrLeuGluPheLeuLysIleProSerThrLeuAlaProProMetAspProSerVal	140
Db	367	CAAACTCTGGAATTTTFAAAAAATCCCTTCCACACTTGACACCCATGGACCATCTGTG	426
QY	141	ProIleTrpIleIlePheGlyValIlePheCysIleIleValAlaIleAlaLeu	160
Db	427	CCCATCTGGATTATTATATTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTA	486
QY	161	LeuIleLeuSerGlyIleTrpGlnArgArgLysAsnLysGluProSerGluValAsp	180
Db	487	CTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACCAATGCAAGTGGAT	546
QY	181	AspAlaGluAspLysCysGluAsnMetIleThrIleGluAsnGlyIleProSerAspPro	200
Db	547	GACGCTGAAGATAAGTGTGAAACCATGATCACAAATTGAAAAATGGCATCCCTCTGATCCC	606
QY	201	LeuAspMetLysGlyGlyIleLeuMetMetProSer	212
Db	607	CTGGACATGAAGGGGGGCATATTAAATGATGCCTTCA	642

RESULT 10
US-09-993-604-386
; Sequence 386, Application US/09993604
; Patent No. US20020137075A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
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; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730PIC25
; CURRENT APPLICATION NUMBER: US/09/993,604
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066770
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/075945
; PRIOR FILING DATE: 1998-02-25
; PRIOR APPLICATION NUMBER: 60/078910

; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091633
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Alignment Scores:

Pred. No.:	3,65e-147	Length:	1346
Score:	1102.00	Matches:	212
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	9	Gaps:	0

US-09-989-724-387 (1-212) x US-09-993-604-386 (1-1346)

QY 1 MetLeuTrpLeuLeuPhePheLeuValThrAlaIleHisAlaGluLeuCysGlnProGly 20
Db 7 AAGTTGGTGGCTGCTCTTTTCTGTGAGCTGCCATTGCTGAACTCTGTCAACAGGT 66
QY 21 AlaGluAsnAlaPheLysValArgLeuSerIleArgThrAlaLeuGlyAspLysAlaTyr 40
Db 67 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 126
QY 41 AlaTrpAspThrAsnGluGluTyrLeuPheLysAlaMetValAlaPheSerMetArgLys 60
Db 127 GCCTGGGATACCAATGAAGAATACCTCTTCAAGCGATGGTAGCTTCTCCATGAGAAA 186
QY 61 ValProAsnArgGluAlaThrGluIleSerHisValLeuLeuCysAsnValThrGlnArg 80
Db 187 GTTCCCAACAGAGAACAGCAAGAAATTTCCATGCTCTACTTTGCAATGTAAACCCAGAG 246
QY 81 ValSerPheTrpPheValValThrAspProSerLysAsnHisThrLeuProAlaValGlu 100
Db 247 GTATCATTTCTGTTTGTGTTTACAGACCTTCAAAAATCAGACCTTCTCTGCTGTGAG 306
QY 101 ValGlnSerAlaIleArgMetAsnLysAsnArgIleAsnAsnAlaPhePheLeuAsnAsp 120
Db 307 GTGCAATCAGCCATGAAGAATGAACAAGAACCGGATCAACAATGCCCTCTTTCTAAATGAC 366
QY 121 GlnThrLeuGluPheLeuLysIleProSerThrLeuAlaProProMetAspProSerVal 140
Db 367 CAAACTCTGGAATTTTAAAAATCCCTTCCACATTCACACCCACCCATGCCATCTGTG 426
QY 141 ProIleTrpIleIleIlePheGlyValIlePheCysIleIleIleValAlaIleAlaLeu 160
Db 427 CCCATCTGGATTATTATATTTTGGTGTGATATTTTGGATCATCATAGTTGCAATTGACTA 486
QY 161 LeuIleLeuSerGlyIleTrpGlnArgArgArgLysAsnLysGluProSerGluValAsp 180
Db 487 CTGATTTTATCAGGATCTGGCAACGTAGAAGAAACAAGAACCAATCTGAAGTGGAT 546
QY 181 AspAlaGluAspLysCysGluAsnMetIleThrIleGluAsnGlyIleProSerAspPro 200
Db 547 GACCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCTCTGATCCC 606
QY 201 LeuAspMetLysGlyIleLeuMetMetProSer 212
Db 607 CTGGACATGAAGGGGGGCATATTATGATGCCTTCA 642

RESULT 11

US-09-990-456-386
; Sequence 386, Application US/09990456
; Patent No. US20020137890A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc

; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas P.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730P1C22
; CURRENT APPLICATION NUMBER: US/09/990,456
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
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; PRIOR APPLICATION NUMBER: 60/065186
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; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Alignment Scores:

Pred. No.:	3.65e-147	Length:	1346
Score:	1102.00	Matches:	212
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	9	Gaps:	0

US-09-989-724-387 (1-212) x US-09-990-456-386 (1-1346)

Qy	1	MetLeuTrpLeuLeuPheLeuValThrAlaIleHisAlaGluLeuCysGlnProGly	20
Db	7	ATGTTGGCTGCTCTTTTCTGGTGACTGCCATTCTGCTGAACCTCTGTCAACCCAGGT	66
Qy	21	AlaGluAsnAlaPheLysValArgLeuSerIleArgThrAlaLeuGlyAspLysAlaTyr	40
Db	67	GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT	126
Qy	41	AlaTrpAspThrAsnGluTyrLeuPheLysAlaMetValAlaPheSerMetArgLys	60
Db	127	GCCTGGGATACCAATGAAGATACCTCTTCAAGCGATGGTAGCTTCTCCATGAGAAA	186
Qy	61	ValProAsnArgGluAlaThrGluIleSerHisValLeuLeuCysAsnValThrGlnArg	80
Db	187	GTTCCCAACAGAGAGCAACAGAAATTTCCCATGTCTTACTTGTCAATGTAAACCCAGAGG	246

Qy 81 ValSerPheTrpPheValThrAspProSerLysAsnHisThrLeuProAlaValGlu 100
Db 247 GTATCATCTGGTTGTGGTTACAGACCCCTTCAAAAATCACACCCCTTCTGCTGTGAG 306
Qy 101 ValGlnSerAlaIleArgMetAsnLysAsnArgIleAsnAsnAlaPhePheLeuAsnAsp 120
Db 307 GTGCAATCAGCCATAAGATGAACAAGAACCGGATCAACATGCCTTCTTCTAAATGAC 366
Qy 121 GlnThrLeuGluPheLeuLysIleProSerThrLeuAlaProProMetAspProSerVal 140
Db 367 CAAACTCTGAATTTTAAATAATCCCTTCCACACTTGGACCAACCCATGGACCATCTGTG 426
Qy 141 ProIleTrpIleIleIlePheGlyValIlePheCysIleIleIleValAlaIleAlaLeu 160
Db 427 CCCATCTGGATTATTATATTGGTGTGATTTTGCATCATCATAGTTGCAATTGCACATA 486
Qy 161 LeuIleLeuSerGlyIleTrpGlnArgArgLysAsnLysGluProSerGluValAsp 180
Db 487 CTGATTTTATCAGGGATCTGGCAACGTAGAAAGAACAAAGAACCATCTGAAGTGGAT 546
Qy 181 AspAlaGluAspLysCysGluAsnMetIleThrIleGluAsnGlyIleProSerAspPro 200
Db 547 GACGCTGAAGATAAGTGTGAACATGATCACAATTGAAATGGCATCCCTCTGTATCCC 606
Qy 201 LeuAspMetLysGlyGlyIleLeuMetMetProSer 212
Db 607 CTGGACATGAAGGGGGGCATATTAAATGATGCCTTCA 642

RESULT 12

US-09-989-721-386
; Sequence 386, Application US/09989721
; Patent No. US20020142961A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary B.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C55
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; PRIOR APPLICATION NUMBER: 60/049787
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; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Alignment Scores:
Pred. No.: 3.6Se-147 Length: 1346
Score: 1102.00 Matches: 212
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-09-989-724-387 (1-212) x US-09-989-721-386 (1-1346)

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Qy 21 AlaGluAsnAlaPheLysValArgLeuSerIleArgThrAlaLeuGlyAspLysAlaTyr 40
Db 67 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 126

Qy 41 AlaTrpAspThrAsnGluGluTyrLeuPheLysAlaMetValAlaPheSerMetArgLys 60
Db 127 GCCTGGGATACCAATGAAGATACCTCTTCAAGCGATGGTAGCTTTCTCCATGAGAAAA 186

Qy 61 ValProAsnArgGluAlaThrGluIleSerHisValLeuLeuCysAsnValThrGlnArg 80
Db 187 GTTCCCAACAGAGAGAGCAACAGAAATTTCCCATGTCTTCAATGTAAACCCAGAGG 246

Qy 81 ValSerPheTrpPheValValThrAspProSerLysAsnHisThrLeuProAlaValGlu 100
Db 247 GTATCATCTGGTTTGGTTTACAGACCTTCAAAAAATCACACCTTTCCTGCTGTTGAG 306

Qy 101 ValGlnSerAlaIleArgMetAsnLysAsnArgIleAsnAsnAlaPhePheLeuAsnAsp 120
Db 307 GTGCAATCAGCCATAGAATGAACAAGAACCGGATCAACATGCTTCTTTCTAAATGAC 366

Qy 121 GlnThrLeuGluPheLeuLysIleProSerThrLeuAlaProProMetAspProSerVal 140
Db 367 CAAACTCTGGAATTTTAAAAATCCCTTCCACACTTGCACACCCATGGACCCATCTGTG 426

Qy 141 ProIleTrpIleIleIlePheGlyValIlePheCysIleIleIleValAlaIleAlaLeu 160
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Qy 161 LeuIleLeuSerGlyIleTrpGlnArgArgLysAsnLysGluProSerGluValAsp 180
Db 487 CTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCAATCTGAAGTGGAT 546

Qy 181 AspAlaGluAspLysCysGluAsnMetIleThrIleGluAsnGlyIleProSerAspPro 200
Db 547 GACGCTGAAGATAAGTGTGAAGAACATGATCACAATTTGAAATGGCATCCCTCTGATCCC 606

Qy 201 LeuAspMetLysGlyGlyIleLeuMetMetProSer 212
Db 607 CTGGACATGAAGGGGGGCATATTATATGATGCCTTCA 642

RESULT 13
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; Sequence 386, Application US/09992598
; Patent No. US20020160384A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.

; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
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; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730PIC20
; CURRENT APPLICATION NUMBER: US/09/992,598
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; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089538
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089598
; PRIOR FILING DATE: 1998-06-17
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; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/091478
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091544
; PRIOR FILING DATE: 1998-07-01
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; PRIOR FILING DATE: 1998-07-02
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; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091633
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Alignment Scores:
Pred. No.: 3.65e-147 Length: 1346
Score: 1102.00 Matches: 212
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-09-989-724-387 (1-212) x US-09-992-598-386 (1-1346)

Qy 1 MetLeuTrpLeuPheLeuValThrAlaIleHisAlaGluLeuCysGlnProGly 20
Db 7 ATGTTGGCTGCTCTTTTCTGGTGACTGCCATTCAGTGAACCTGTCAACAGGT 66
Qy 21 AlaGluAsnAlaPheLysValArgLeuSerIleArgThrAlaLeuGlyAspLysAlaTyr 40
Db 67 GCAGAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 126
Qy 41 AlaTrpAspThrAsnGluGluTyrLeuPheLysAlaMetValAlaPheSerMetArgLys 60
Db 127 GCCTGGGATACCAATGAAGAATACCTCTTCAAGCGATGCTAGCTTTCTCCATGAGAAA 186

Qy 61 ValProAsnArgGluAlaThrGluIleSerHisValLeuLeuCysAsnValThrGlnArg 80
Db 187 GTTCCCAACAGAGAACAGAAATTTCCCATGTCTCTTGTCAATGTAAACCCAGAGG 246
Qy 81 ValSerPheTrpPheValValThrAspProSerLysAsnHisThrLeuProAlaValGlu 100
Db 247 GTATCAATCTGGTTTGTGGTTACAGACCTTCAAAAAATCACACCCCTTCTCTGCTTTGAG 306
Qy 101 ValGlnSerAlaIleArgMetAsnLysAsnArgIleAsnAsnAlaPhePheLeuAsnAsp 120
Db 307 GTGCAATCAGCCCATAGAATGAACAAGAACCCGGATCAACAATGCCCTTCTTTCTAAATGAC 366
Qy 121 GlnThrLeuGluPheLeuLysIleProSerThrLeuAlaProProMetAspProSerVal 140
Db 367 CAAACTCTGGAAATTTTAAAAAATCCCTTCCACACTTGCAACCCCATGGACCCCATCTGTG 426
Qy 141 ProIleTrpIleIleIlePheGlyValIlePheCysIleIleIleValAlaIleAlaLeu 160
Db 427 CCCATCTGGATTATTATATTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACATA 486
Qy 161 LeuIleLeuSerGlyIleTrpGlnArgArgArgLysAsnLysGluProSerGluValAsp 180
Db 487 CTGATTTTATCAGGGATCTGGCAACGTAGAAAGAAAGAACAAAGAACCATCTGAAAGTGGAT 546
Qy 181 AspAlaGluAspLysCysGluAsnMetIleThrIleGluAsnGlyIleProSerAspPro 200
Db 547 GACGCTGAAGATAAGTGTGAAGAACATGATCAACAATTGAAATGGCATCCCTCTGTATCCC 606
Qy 201 LeuAspMetLysGlyGlyIleLeuMetMetProSer 212
Db 607 CTGGACATGAAGGGGGGCATATTATATGATGCCCTTCA 642

RESULT 14

US-09-989-293A-386
; Sequence 386, Application US/09989293A
; Patent No. US20020177164A1
; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; Acids Encoding the Same
; FILE REFERENCE: P2730P1C66

; CURRENT APPLICATION NUMBER: US/09/989,293A
; CURRENT FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/065311

[illegible]

; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091544
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/091519
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091626
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091633
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Alignment Scores:
Pred. No.: 3.65e-147 Length: 1346
Score: 1102.00 Matches: 212
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-09-989-724-387 (1-212) x US-09-989-293A-386 (1-1346)

Qy	1	MetLeuTrpLeuLeuPhePheLeuValThrAlaIleHisAlaGluLeuCysGlnProGly	20
Db	7	ATGTTGGTGCTCTTTTCTGGTGACTGCCATTTCATGCTGAACTCTGTCAACCGGT	66
Qy	21	AlaGluAsnAlaPheLysValArgLeuSerIleArgThrAlaLeuGlyAspLysAlaTyr	40
Db	67	GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGAGATAAAGCATAT	126
Qy	41	AlaTrpAspThrAsnGluTyrLeuPheLysAlaMetValAlaPheSerMetArgLys	60
Db	127	GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAA	186
Qy	61	ValProAsnArgGluAlaThrGluIleSerHisValLeuLeuCysAsnValThrGlnArg	80
Db	187	GTTCCCAACAGAGNAGCAACAGAAATTTCCCATGTCTTCTACTTTGCAATGTAAACCCAGAG	246
Qy	81	ValSerPheTrpPheValValThrAspProSerLysAsnHisThrLeuProAlaValGlu	100
Db	247	GTATCATTTCTGGTTTGTGGTTACAGACCTTCAAAAAATCACACCTTCTCTGCTGTGAG	306
Qy	101	ValGlnSerAlaIleArgMetAsnLysAsnArgIleAsnAsnAlaPhePheLeuAsnAsp	120
Db	307	GTGCAATCAGCCCATAGATGAACAGACCGGATCAACAATGCCCTTCTTTCTAAATGAC	366
Qy	121	GlnThrLeuGluPheLeuLysIleProSerThrLeuAlaProProMetAspProSerVal	140
Db	367	CAAACTCGGAATTTTAAAAATCCCTTCCACACTTGCACCCATGGACCCCATCTGTG	426
Qy	141	ProIleTrpIleIleIlePheGlyValIlePheCysIleIleValAlaIleAlaLeu	160
Db	427	CCCATCTGGATTATTATATTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTA	486
Qy	161	LeuIleLeuSerGlyIleTrpGlnArgArgLysAsnLysGluProSerGluValAsp	180
Db	487	CTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAAGTGGAT	546
Qy	181	AspAlaGluAspLysCysGluAsnMetIleThrIleGluAsnGlyIleProSerAspPro	200
Db	547	GACGCTGAAGATAAGTGTGAACAACATGATCACAATTTGAAAATGGCATCCCTCTGATCCC	606
Qy	201	LeuAspMetLysGlyIleLeuMetMetProSer	212
Db	607	CTGGACATGAAGGGGGGCATATTAAATGATGCCTTCA	642

RESULT 15

US-09-989-735-386

; Sequence 386, Application US/09989735

; Publication No. US20020193299A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas P.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C61
; CURRENT APPLICATION NUMBER: US/09/989,735
; CURRENT FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
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 ; PRIOR APPLICATION NUMBER: 60/091633
 ; PRIOR FILING DATE: 1998-07-02
 ; PRIOR APPLICATION NUMBER: 60/091778
 ; PRIOR FILING DATE: 1998-07-07
 ; PRIOR APPLICATION NUMBER: 60/091982
 ; PRIOR FILING DATE: 1998-07-07
 ; PRIOR APPLICATION NUMBER: 60/092182
 ; PRIOR FILING DATE: 1998-07-09

Alignment Scores:

Pred. No.:	3,65e-147	Length:	1346
Score:	1102.00	Matches:	212
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	9	Gaps:	0

US-09-989-724-387 (1-212) x US-09-989-735-386 (1-1346)

Qy	1	MetLeuTyrLeuLeuPhePheLeuValThrAlaIleHisAlaGluLeuCysGlnProGly	20
Db	7	ATGTTGTGGCTCTCTTTTCTGGTGACTGCCATTCATGCTGTAAGTCTGTCAACAGGT	66
Qy	21	AlaGluAsnAlaPheLysValArgLeuSerIleArgThrAlaLeuGlyAspLysAlaTyr	40
Db	67	GCAGAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAGCATAT	126
Qy	41	AlaTrpAspThrAsnGluGluTyrLeuPheLysAlaMetValAlaPheSerMetArgLys	60

Db	127	GCCTGGGATACCAATGAAGATACCTCTTCAAGCGATGGTAGCTTTCTCCATGAGAAAA	186
Qy	61	ValProAsnArgGluAlaThrGluIleSerHisValLeuLeuCysAsnValThrGlnArg	80
Db	187	GTTCCTCCACAGAGAGCAACAGAAATTTCCCATGTCTTACTTTGCAATGTAAACCCAGAGG	246
Qy	81	ValSerPheTrpPheValValThrAspProSerLysAsnHisThrLeuProAlaValGlu	100
Db	247	GTATCAATCTGGTTTGTGGTTACAGACCCCTTCAAAAAATCACACCCCTTCTGCTGTTGAG	306
Qy	101	ValGlnSerAlaIleArgMetAsnLysAsnArgIleAsnAsnAlaPhePheLeuAsnAsp	120
Db	307	GTGCAATCAGCCATAAGATGAACAAGACCGGATCAACAATGCCCTTCTTCTAAATGAC	366
Qy	121	GlnThrLeuGluPheLeuLysIleProSerThrLeuAlaProProMetAspProSerVal	140
Db	367	CAAACTCTGGAAATTTTAAAAATCCCTTCCACACTTGCACCCCATGGACCCATCTGTG	426
Qy	141	ProIleTrpIleIleIlePheGlyValIlePheCysIleIleIleValAlaIleAlaLeu	160
Db	427	CCCATCTGGATTATTATATTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACATA	486
Qy	161	LeuIleLeuSerGlyIleTrpGlnArgArgArgLysAsnLysGluProSerGluValAsp	180
Db	487	CTGATTTTATCAGGGATCTGGCAACGTAGAGAAAGAACAAAGAACCAATCTGAAGTGGAT	546
Qy	181	AspAlaGluAspLysCysGluAsnMetIleThrIleGluAsnGlyIleProSerAspPro	200
Db	547	GACGCTGAAGATAAGTGTGAANAACATGATCACAAATTGAANAATGGCATCCCTCTGATCCC	606
Qy	201	LeuAspMetLysGlyGlyIleLeuMetMetProSer	212
Db	607	CTGGACATGAAGGGGGGCATATTAAATGATGCCTTCA	642

Search completed: April 4, 2004, 05:10:36
Job time : 417 secs

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Db 74 ITTFLVR--PNCEAIKTPHQFRILFMDHTIVTSSTPRETGLLNKFTFPDYIVDDVVGND 131
QY 95 TLPAVEVQSAIRMNKNRINNAPFLNDQTLFLKIPSTL 132
Db 132 TL--VDVIGAL-VNVGIMTNT-ASNENDMAGFKLPFTI 165

RESULT 6
D38992
cadherin 8 - human
C:Species: Homo sapiens (man)
C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jan-2000
C:Accession: D38992
R:Suzuki, S.; Sano, K.; Tanihara, H.
Cell Regul. 2, 261-270, 1991
A:Title: Diversity of the cadherin family: evidence for eight new cadherins in nervous t
A:Reference number: S24305; MUID:91283540; PMID:2059658
A:Accession: D38992
A:Status: preliminary; translated from GB/EMBL/DBBJ
A:Molecule type: mRNA
A:Residues: 1-793 <SUZ>
A:Cross-references: GB:L34060; NID:g506411; PIDN:AAA35628.1; PID:g506412
C:Genetics:
A:Gene: GDB:CDH8
A:Cross-references: GDB:5822911
C:Superfamily: cadherin; cadherin repeat homology
C:Keywords: calcium binding; cell adhesion; duplication
F;163-269/Domain: cadherin repeat homology <CDH>

Query Match 8.1%; Score 89.5; DB 2; Length 793;
Best Local Similarity 20.5%; Pred. No. 3.5;
Matches 50; Conservative 35; Mismatches 93; Indels 65; Gaps 10;
QY 13 HAEQCQPGAENAFKVRLSIRTALGDKAYAWDT-----NEEYLFKAMVAFSMRKVPN 63
Db 425 HTDLERQFNINADGKITLATPLDRLSVWHNITITATEIRNHSQISRVPVAIKVLDV-N 483
QY 64 REATEIS--HVLCC-----NVTORVSFWFVWTDPSKNH-----TLPAVEVQSAIRMNK 109
Db 484 DNAPEFASEYEAFLECKGKPGQVIQTVSA-MDKDDPKNGHYFLYSLLPENMVNPNFTIKK 542
QY 110 NRINNAPFL-----NDQTLFLKIPSTLA---PMDPSVPIWIIIFG----- 148
Db 543 NEDNSLSILAKHNGFNQKQEVYLLPIIISDSGNPPLSSTLTITRVCGSNDGVVQSCN 602
QY 149 -----VIFCIIIVAIALLILSGIWRKKNKEPSEVDDAEDKCNEMIT 191
Db 603 VEAYVLPIGLSMGALITAILACIILLVIVWLF--VTLRRHQKNEPLIKDDEDVRENIIR 660
QY 192 IEN 194
Db 661 YDD 663

RESULT 7
T13933
pol polyprotein - fruit fly (Drosophila virilis) retrotransposon Tv1 (fragment)
C:Species: Drosophila virilis
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 17-Nov-2000
C:Accession: T13933
R:Andrianov, B.V.; Zakharyev, V.M.; Evgen'ev, M.B.; Schuppe, N.G.
submitted to the EMBL Data Library, April 1998
A:Description: Gypsy group retrotransposon Tv1 from Drosophila virilis.
A:Reference number: Z17816
A:Accession: T13933
A:Status: preliminary; translated from GB/EMBL/DBBJ
A:Molecule type: DNA
A:Residues: 1-1188 <AND>
A:Cross-references: EMBL:AF056940; NID:g3493212; PID:g3493214; PIDN:AAC33318.1
C:Genetics:

A:Gene: pol
A:Cross-references: FlyBase:FBgn0013099
A:Mobile element: retrotransposon Tv1
C:Superfamily: pol polyprotein

Query Match 8.1%; Score 89.5; DB 2; Length 1188;
Best Local Similarity 24.8%; Pred. No. 5.6;
Matches 34; Conservative 27; Mismatches 41; Indels 35; Gaps 7;
QY 5 LFFLVTAIHAELCQPGAENAFKVRLSIRTALGDKAYAWDTNBEYLFKAMVAFSMRKVPNR 64
Db 81 LNYQISPIHAECTKPS-----RLTSRDSNSGOIRIWNIGKFL-----PSKPREPNR 127
QY 65 EAT-----EISHVLLCNV-----TORVSFWFVWTDPSKNHTLPAV-EVQSAIR 106
Db 128 NKSIHKWIMELTKFLKCVIDTGTSTINLMKTNRLNF-PVYNETLKVHTINGVIELKQSIR 186
QY 107 MNKNRI---NNAFFLND 120
Db 187 LGASKICPSKQKFIYHD 203

RESULT 8
JC7294
alphan integrin - sea urchin (Strongylocentrotus purpuratus)
C:Species: Strongylocentrotus purpuratus (purple urchin)
C:Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 02-Sep-2000
C:Accession: JC7294
R:Susan, J.M.; Just, M.L.; Lennarz, W.J.
Biochem. Biophys. Res. Commun. 272, 929-935, 2000
A:Title: Cloning and characterization of alphan integrin in embryos of the sea urchin
A:Reference number: JC7294
A:Contents: Embryo
A:Accession: JC7294
A:Molecule type: mRNA
A:Residues: 1-1054 <SUS>
A:Cross-references: GB:AAD55724
C:Genetics:
A:Gene: aualphap
C:Superfamily: integrin alpha-2b chain
C:Keywords: calcium binding; embryo; glycolysis; glycoprotein; heterodimer; transmembr

Query Match 8.1%; Score 89; DB 2; Length 1054;
Best Local Similarity 20.5%; Pred. No. 5.4;
Matches 56; Conservative 30; Mismatches 59; Indels 128; Gaps 13;
QY 15 ELCQPGAENAFKVRLSIRTALGDKAYAW---DTNBEYLF----- 50
Db 795 EVRNTGSSNAAEVTNIR-----WPEKDENGDLFYLLGIMTDEGVTQISQSQAN 845
QY 51 -----KAMVAFSMRKVPNRE-----ATEISHVLL-CNVVQ--- 79
Db 846 PLGVKLEASTKBQLSNSTTQVSGRRKREGEYAEALAAQAEPIFCTPESCVLINCTIDEIKA 905
QY 80 -----RV--SFVFWVTDPSKNHTLPAVEVQSAIRMNKNRINNAPFLNDQTLFLKIPST 131
Db 906 TKSQVVRILGRFWERTFQKAVSEAVPVIQVTLA-----STATATVRSIPYN 951
QY 132 LAPMD-----PSVPI--WIIIFGVIFCIIIVAIALLILSGIWQ--- 168
Db 952 IPLPMEFTDSTKASTLITAEELVLPVPSIAWIIIVSVLGGIILL---LIILGLWKCGF 1008
QY 169 -RRKNKE-----PSEVDDAEDK 185
Db 1009 PERKKPGEDQKEVEPVAVTEKDGPEVVDAPDR 1041

RESULT 9
A37009
CD44 homolog membrane glycoprotein precursor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 31-Jan-1992 #sequence_revision 31-Jan-1992 #text_change 21-Jul-2000
C:Accession: A37009

C;Genetics:
A;Map position: 3
A;Note: F18N11.180
C;Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolo

Query Match 7.8%; Score 85.5; DB 2; Length 667;
Best Local Similarity 21.6%; Pred. No. 6.6;
Matches 37; Conservative 23; Mismatches 64; Indels 47; Gaps 6;

QY 81 VSFVFWVTDPSKNHTLPAVEVQSAIR-----MKNKRINNAPF 117
DB 192 VQWIDYDGLNLNVTLPAPIEQPNRPLISRDINLSEIFQDKMYIGSGNGLTSNQYI 251

QY 118 LN-----DQTLBFLKIPSTLAP-----PMDPSVPIWIIIFGVIFCIIIVAIALL 161
DB 252 LGWSFSKSKFMSQLDLSKLPQAPIRNEQAPVPREKKLHPLLLGLV--ILLVIPVLM 309

QY 162 ILSGI-WQRRRNKKEPSEVDDAE-----DKCENMITIENGIPSDPLDMKGG 206
DB 310 VLGGVWYRRKKYAEVKESWEKEYGPHRYSYKSLYKATNGFVKDALVGKGG 360

RESULT 14
E81924
Probable two-component system sensor kinase (EC 2.7.3.-) NMA0797 [imported] - Neisseria
C;Species: Neisseria meningitidis
C;Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 02-Feb-2001
C;Accession: E81924
R;Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel
; Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream,
Nature 404, 502-506, 2000
A;Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491.
A;Reference number: A81775; MUID:20222556; PMID:10761919
A;Accession: E81924
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-468 <PAR>
A;Cross-references: GB:AL162754; GB:AL157959; NID:g7379424; PIDN:CAB84080.1; PID:g737951
A;Experimental source: serogroup A, strain Z2491
C;Genetics:
A;Gene: NMA0797
C;Keywords: phosphotransferase

Query Match 7.7%; Score 84.5; DB 2; Length 468;
Best Local Similarity 23.7%; Pred. No. 5.4;
Matches 47; Conservative 29; Mismatches 81; Indels 41; Gaps 9;

QY 21 AENAPKVRLSIRTAL-----GDKAYAWDTNEEYLFKAMVAFSMRKVPNREATEI 69
DB 34 AENQFNQRTIETLMGSIISAFRAGD-AGAREILTEWK-DSPVSSGVYVIQDSEKKOI 91

QY 70 SHVLLCNVTQRFVFWVTDPSKNHTLPAVEVQSAIRMNKNRINN--AFFLND-QTLEFL 126
DB 92 LHRVIDSYTIERARLFAAGPHSN-----LVHIEYDRFGEEYLFFTKDWKLOAR 141

QY 127 KIPSTLAPPMDPSVPIW-----IIIFGVIFCII--VAIALLILSGIWQR-----RR 171
DB 142 RLPSPLLIPLGLPAPIWHELIILSPIIIVGLLMAYILAGNIAPRILGNGMDRVANGEL 201

QY 172 KNKEPSEVDDAEKCNM 189
DB 202 ETRISQQVDDRDELSHL 219

RESULT 15
JG0022
Flagellar basal-body M-ring protein fliP - Bacillus subtilis
C;Species: Bacillus subtilis
C;Date: 23-Nov-1991 #sequence_revision 23-Nov-1991 #text_change 21-Jul-2000
C;Accession: JG0022; A42365; B69624; S14494
R;Zuberi, A.R.; Ying, C.; Bischoff, D.S.; Ordal, G.W.
Gene 101, 23-31, 1991
A;Title: Gene-protein relationships in the flagellar hook-basal body complex of Bacillus

A;Reference number: JG0019; MUID:91285431; PMID:1905667
A;Accession: JG0022
A;Molecule type: DNA
A;Residues: 1-536 <ZUB>
A;Cross-references: GB:M54965
R;Albertini, A.M.; Caramori, T.; Crabb, W.D.; Scoffone, F.; Galizzi, A.
J. Bacteriol. 173, 3573-3579, 1991
A;Title: The flmA locus of Bacillus subtilis is part of a large operon coding for flag
A;Reference number: A42365; MUID:91258343; PMID:1828465
A;Accession: A42365
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 355-536 <ALB>
A;Cross-references: GB:M72718; EMBL:X56049; NID:g39904; PIDN:CAA39520.1; PID:g3979709
R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berc
C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; C
A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Brington, J.; Fabret, C.; Ferrari, E
Nature 390, 249-256, 1997
A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gall
iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.
Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois
A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mauel
Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetel
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadie, Y.; Sato, T.; Scanlon
A;Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Ser
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchlyam
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida,
A;Authors: Yoshikawa, H.F.; Zumstein, B.; Yoshikawa, H.; Danchin, A.
A;Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis
A;Reference number: A69580; MUID:98044033; PMID:9384377
A;Accession: B69624
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-536 <KUN>
A;Cross-references: GB:Z99112; GB:AL009126; NID:g2633902; PIDN:CAB13494.1; PID:e118521;
A;Experimental source: strain 168
C;Genetics:
A;Gene: flfP

Query Match 7.7%; Score 84.5; DB 2; Length 536;
Best Local Similarity 19.9%; Pred. No. 6.3;
Matches 39; Conservative 36; Mismatches 68; Indels 53; Gaps 8;

QY 9 VTAIHAELOCQGAENAPKVRLSIRTALGDKAYAWDTNEEYLFKAMVAFSMRKVPNREATE 68
DB 352 VNRIHKEI-----AESPYKVR-----DLGIQVMVEPPDAKNTASLSTERQDD 393

QY 69 ISHVLLCNVTQRFVFWVTDPSKNHTLPAVEVQSAIRMNKNRINNAPFLNDQTLEFLKI 128
DB 394 IQKIL--STVVRTS---LDKDETQNLSDADINNKIVSVQPFQDKGNLDTNTE--- 444

QY 129 PSTLAPPMDPSVPIW-IIIFGVIFCIIIVAIALLILSGIWQRRRNKKEPSEVDDAEKCE 187
DB 445 -----SSGIPLWAYIVGGVLIAAIIVLIIMLI-----RKRAQDEFESEYE-- 487

QY 188 NMITIENGIPSDPLDM 203
DB 488 -----VPQBPINL 495

Search completed: March 31, 2004, 12:07:17
Job time : 23 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 31, 2004, 12:02:04 ; Search time 18 Seconds
(without alignments)
613.271 Million cell updates/sec

Title: US-09-989-724-387

Perfect score: 1102

Sequence: 1 MLWLLPFLVTAHAEACQPG.....ENGIPSDPLDMKGILMPS 212

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	92.5	8.4	1153	1 NOS_LYMST	O61309 lymnaea sta
2	91	8.3	623	1 SYR_SULTO	Q971x1 sulfolobus
3	90	8.2	799	1 CAD8_MOUSE	P97291 mus musculus
4	90	8.2	799	1 CAD8_RAT	O54800 rattus norv
5	89.5	8.1	1025	1 ITAB_HUMAN	P53708 homo sapien
6	89	8.1	799	1 CAD8_HUMAN	P55286 homo sapien
7	88	8.0	778	1 CD44_MOUSE	P15379 mus musculus
8	87	7.9	362	1 CD44_CHICK	P20944 cricetus
9	86	7.8	431	1 CD44_MESAU	Q60522 m cd44 anti
10	86	7.8	503	1 CD44_RAT	P26051 rattus norv
11	84.5	7.7	536	1 FLIF_BACSU	P23447 bacillus su
12	83.5	7.6	1337	1 PTPJ_HUMAN	Q12913 homo sapien
13	82.5	7.5	1044	1 ITAB_CHICK	P26009 gallus gall
14	82	7.4	1189	1 ITAB_HUMAN	Q9ukx5 homo sapien
15	81.5	7.4	363	1 LEU3_PHOLL	Q7n128 photorhabdu
16	81.5	7.4	1048	1 ITAV_HUMAN	P06756 homo sapien
17	81	7.4	1179	1 ITAV_MOUSE	Q61738 mus musculus
18	80.5	7.3	1034	1 ITAV_CHICK	P26008 gallus gall
19	80	7.3	234	1 VGP8_BBV	P03224 epstein-bar
20	79.5	7.2	393	1 IL1S_CERAB	Q29612 cercopithec
21	79.5	7.2	1044	1 ITAV_MOUSE	P43406 mus musculus
22	79	7.2	437	1 YC44_PORPU	P51363 porphyra pu
23	79	7.2	611	1 RBT3_MOUSE	Q9ctn4 mus musculus
24	79	7.2	1033	1 ITAB_MOUSE	Q9qum0 mus musculus
25	79	7.2	2029	1 LAR_DROME	P16621 drosophila
26	78	7.1	343	1 MRGF_RAT	P23749 rattus norv
27	78	7.1	732	1 CADL_CHICK	P33145 gallus gall
28	78	7.1	1022	1 ALAI_ANGAN	Q92030 anguilla an
29	77.5	7.0	351	1 CD44_CANPA	Q28284 canis famil
30	77	7.0	322	1 GPT_SULSO	P96000 sulfolobus
31	76.5	6.9	363	1 LEU3_SALT	P37412 salmonella
32	76.5	6.9	365	1 OPSR_XENLA	Q12948 xenopus lae
33	76.5	6.9	475	1 MUC1_HYLLA	Q29435 hylobates l

ALIGNMENTS

RESULT 1

NOS_LYMST

ID NOS_LYMST STANDARD; PRT; 1153 AA.

AC O61309;

DT 30-MAY-2000 (Rel. 39, Created)

DT 30-MAY-2000 (Rel. 39, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Nitric-oxide synthase (EC 1.14.13.39) (NOS, type I) (Neuronal NOS)

DE (NOS) (nNOS).

GN NOS.

OS Lymnaea stagnalis (Great pond snail).

OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Basommatophora;

OC Lymnaeidae; Lymnaeidae; Lymnaea.

OX NCBI_TaxID=6523;

RN [1]

RP SEQUENCE FROM N.A. (ISOFORMS LONG AND SHORT).

RC TISSUE=CNS;

RX MEDLINE=98211896; PubMed=9552167;

RA Korneev S.A., Piper M.R., Picot J., Phillips R., Korneeva E.I.,

RA O'Shea M.;

RT "Molecular characterization of NOS in a mollusc: expression in a giant modulatory neuron."

RL J. Neurobiol. 35:65-76(1998).

CC -!- FUNCTION: Produces nitric oxide (NO) which is a messenger molecule with diverse functions throughout the body (By similarity).

CC -!- CATALYTIC ACTIVITY: L-arginine + N NADPH + M O(2) = citrulline + nitric oxide + N NADP(+).

CC -!- COFACTOR: Heme. Binds one mole each of FAD and FMN (By similarity).

CC -!- ENZYME REGULATION: Stimulated by calcium/calmodulin.

CC -!- ALTERNATIVE PRODUCTS:

CC Event=Alternative splicing; Named isoforms=2;

CC Name=Long;

CC IsoId=O61309-1; Sequence=Displayed;

CC Name=Short;

CC IsoId=O61309-2; Sequence=VSP_003584;

CC -!- TISSUE SPECIFICITY: Expressed in the central nervous system, in the serotonergic cerebral giant cells. Both the long and short isoforms are expressed equally in the CNS.

CC -!- SIMILARITY: Belongs to the NOS family.

CC -!- SIMILARITY: Contains 1 flavodoxin-like domain.

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CC -----

CC EMBL; AF012531; AAC17487.1; --

CC PIR; T31080; T31080.

CC HSSP; P29477; LDD7.

CC InterPro; IPR003097; PAD_binding.

CC InterPro; IPR008254; Flav_nitox_synth.

CC InterPro; IPR001094; Flavodoxin_like.

DR InterPro; IPR001709; FPN cvt redctse.
DR InterPro; IPR004030; NO_synthase.
DR InterPro; IPR001433; Oxired_FAD(P).
DR Pfam; PF00667; FAD_binding_1; 1.
DR Pfam; PF00258; flavodoxin; 1.
DR Pfam; PF00175; NAD_binding_1; 2.
DR Pfam; PF02898; NO_synthase; 1.
DR PRINTS; PR00369; FLAVODOXIN.
DR PRINTS; PR00371; FPNCR.
DR PROSITE; PS0902; FLAVODOXIN_LIKE; 1.
DR PROSITE; PS6001; NOS; 1.
KW Oxidoreductase; NADP; FAD; FMN; Calmodulin-binding; Heme; Repeat;
KW Alternative splicing.
FT DOMAIN 427 610 FLAVODOXIN-LIKE.
FT METAL 82 82 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
FT DOMAIN 397 417 CALMODULIN-BINDING (POTENTIAL).
FT NP_BIND 556 587 FMN (PYRIMIDINE PART) (BY SIMILARITY).
FT NP_BIND 697 708 FAD (ADP PART) (BY SIMILARITY).
FT NP_BIND 836 846 FAD (FLAVIN PART) (BY SIMILARITY).
FT NP_BIND 911 929 NADP (RIBOSE PART) (BY SIMILARITY).
FT NP_BIND 1089 1104 NADP (ADP PART) (BY SIMILARITY).
FT DOMAIN 934 1010 11 X 7 AA TANDEM REPEATS OF E-[NT]-[ST]-[IM]-P-S-C.
FT VARSPLIC 276 309 Missing (in isoform Short).
FT /FTID=VSP 003584.
SQ SEQUENCE 1153 AA; 129085 MW; 101B77D02B66B109 CRC64;

Query Match 8.4%; Score 92.5; DB 1; Length 1153;
Best Local Similarity 21.1%; Pred.No. 1.7;
Matches 64; Conservative 28; Mismatches 76; Indels 135; Gaps 13;

QY 21 AENAFKVRLSIRLTALGDKAYAWDTNEEYLPKA-MVAFSMRKVPNRE-----ATEI----- 69
Db 689 AHNA-----TDLKYAPGDHVAIFPANSPEIVDAILVRLDTSGPSPDQVVKTEISTQLGTN 744

QY 70 -----SHVLLCNVTQVSFWFVVTDPKSNHTLPAAVEQSAIRMNKNRI-----NNAPF--- 117
Db 745 DTWRSHLPICTSRTAFSFLLDVTTTPSQEILQVLATQASSDMDKHKLEQLASNSEAYEKW 804

QY 118 ---LNDQTLF-----LQIPSTL----- 132
Db 805 RLDLSNILEILDEPESLKIPPSLLLTQLPLLPQPRYSSSQKQNPNEVHATIAVVRPK 864

QY 133 -----AP-----PMDPSVPWIIIFGVIFCIIV 156
Db 865 TDGDGPVHEGVCSWLNRSPIGTVPCLRSAPHFHLPEDPSLPIMIGPG----- 916

QY 157 AIALILSGI-----WQRRRNKKEPSEVDDAKCEN-MITIENGIPSDPLDMKGGILM 209
Db 917 -----SGIAPFRSFQQL-----GEIENTMPSCENTMLSCETTIPSCENSMPSCENT 964

QY 210 MPS 212
Db 965 MPS 967

RESULT 2
SYR_SULTO STANDARD; PRT; 623 AA.
AC Q97IX1;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Arginyl-tRNA synthetase (SC 6.1.1.19) (Arginine--tRNA ligase) (ArgRS).
GN ARGS OR ST1258.
OS Sulfolobus tokodaii.
OC Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
OC Sulfolobus.
OX NCBI_TaxID=111955;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=JCM 10545 / 7;
RX MEDLINE=21456156; PubMed=11572479;

RA Kawarabayasi Y., Hino Y., Horikawa H., Jin-no K., Takahashi M.,
RA Sekine M., Baba S.-I., Ankai A., Kosugi H., Hosoyama A., Fukui S.,
RA Nagai Y., Nishijima K., Otsuka R., Nakazawa H., Takamiya M., Kato Y.,
RA Yoshizawa T., Tanaka T., Kudo Y., Yamazaki J., Kushida N., Oguchi A.,
RA Aoki K.-I., Masuda S., Yanagii M., Nishimura M., Yamagishi A.,
RA Oshima T., Kikuchi H.;
RT *Complete genome sequence of an aerobic thermoacidophilic
RT Crenarchaeon, Sulfolobus tokodaii strain 7.";
RL DNA Res. 8:123-140(2001).
CC -|- CATALYTIC ACTIVITY: ATP + L-arginine + tRNA(Arg) = AMP +
CC diphosphate + L-arginyl-tRNA(Arg).
CC -|- SUBCELLULAR LOCATION: Cytoplasmic.
CC -|- SIMILARITY: Belongs to class-I aminoacyl-tRNA synthetase family.
CC -----
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CC -----
DR EMBL; AP000985; BAB66299.1; -.
DR HAMAP; MP_00123; -; 1.
DR InterPro; IPR001278; Arg tRNA-synt 1c.
DR InterPro; IPR008909; tRNA-synt 1d_C.
DR InterPro; IPR001412; tRNA-synt 1.
DR Pfam; PF00750; tRNA-synt 1d; 1.
DR Pfam; PF05746; tRNA-synt 1d C; 1.
DR PRINTS; PR01038; TRNASYNTHARG.
DR TIGRFAMs; TIGR00456; args; 1.
DR PROSITE; PS00178; AA tRNA LIGASE I; FALSE NEG.
KW Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
KW Complete proteome.
FT SITE 116 126 "HIGH" REGION.
SQ SEQUENCE 623 AA; 71692 MW; A24645D0996B038B CRC64;

Query Match 8.3%; Score 91; DB 1; Length 623;
Best Local Similarity 22.1%; Pred.No. 1.1;
Matches 45; Conservative 31; Mismatches 44; Indels 84; Gaps 12;

QY 45 NEEYLFKAMVA-----FSMRKVPNREATEISHVLLCNVTQVSFWFVVTDPKSNHTLPV 99
Db 82 NESELFKLIFTNFPEDYGIEKIQKQPVVVEH-----TSANPIHPLHVG 125

QY 100 EVQSAI-----RMNKNR---INNAFLNDQ-----TLEPLKI---ESTLAPMDPSVP 141
Db 126 HLRNAILGVDVIARMLKARGHEVNTFRFYNDAGRQVAITLTGYLLLGEPN---PPRDEKID 182

QY 142 IWIIFGVIFCI--IIVAI-----ALLILSGIWQRRRNKBP 176
Db 183 QWI---GVYIAITNIIIEINQLKKEISSSNEEYRQKISKLDLISLAG-----KHREKYP 235

QY 177 -----SEVDDAEDKCNMI 190
Db 236 EIFDKLADEISKIENIEKIQNI 259

RESULT 3
CAD8_MOUSE STANDARD; PRT; 799 AA.
ID CAD8_MOUSE
AC P97291;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Cadherin-8 precursor.
GN CDH8.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.

RESULT 6
 CAD8 HUMAN STANDARD; PRT; 799 AA.
 AC P55286; Q9ULB2;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DE 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Cadherin-8 precursor.
 GN CDH8.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX PubMed=10861224;
 RA Shimoyama Y., Tsujimoto G., Kitajima M., Natori M.;
 RT "Identification of three human type-II classic cadherins and frequent
 RT heterophilic interactions between different subclasses of type-II
 RT classic cadherins.";
 RL Biochem. J. 349:159-167(2000).
 RN [2]
 RP SEQUENCE OF 7-799 FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=95073006; PubMed=7982033;
 RA Tanihara H., Sano K., Heilmann R.L., St John T., Suzuki S.;
 RT "Cloning of five human cadherins clarifies characteristic features of
 RT cadherin extracellular domain and provides further evidence for two
 RT structurally different types of cadherin.";
 RL Cell Adhes. Commun. 2:15-26(1994).
 RN [3]
 RP SEQUENCE OF 294-799 FROM N.A.
 RC TISSUE=Fetal brain;
 RX MEDLINE=91283540; PubMed=2059658;
 RA Suzuki S., Sano K., Tanihara H.;
 RT "Diversity of the cadherin family: evidence for eight new cadherins
 RT in nervous tissue.";
 RL Cell Regul. 2:261-270(1991).
 CC -!- FUNCTION: Cadherins are calcium dependent cell adhesion proteins.
 CC They preferentially interact with themselves in a homophilic
 CC manner in connecting cells; cadherins may thus contribute to the
 CC sorting of heterogeneous cell types.
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- TISSUE SPECIFICITY: Mainly expressed in brain. Found in certain
 CC nerve cell lines, such as retinoblasts, glioma cells and
 CC neuroblasts.
 CC -!- SIMILARITY: Contains 5 cadherin domains.
 CC
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 CC
 CC EMBL; AB035305; BAA87419.1; -.
 CC EMBL; L34060; AAA35628.1; ALT_INIT.
 CC HSSP; P15116; INCJ.
 CC Genew; HGNC:1767; CDH8.
 CC MIM; 603008; -.
 CC GO; GO:0007155; P:cell adhesion; TAS.
 CC InterPro; IPR002126; Cadherin.
 CC InterPro; IPR000233; Cadherin_C_term.
 CC Pfam; PF01049; cadherin; 5.
 CC PRINTS; PR0205; CADHERIN.
 CC SMART; SM00112; CA; 5.
 CC PROSITE; PS00232; CADHERIN_1; 3.
 CC PROSITE; PS0268; CADHERIN_2; 5.
 CC Cell adhesion; Glycoprotein; Transmembrane; Calcium-binding; Repeat;
 CC Signal.

FT SIGNAL 1 29 POTENTIAL.
 FT PROPEP 30 61 POTENTIAL.
 FT CHAIN 62 799 CADHERIN-8.
 FT DOMAIN 62 621 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 622 642 POTENTIAL.
 FT DOMAIN 643 799 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 62 167 CADHERIN 1.
 FT DOMAIN 168 276 CADHERIN 2.
 FT DOMAIN 277 391 CADHERIN 3.
 FT DOMAIN 392 494 CADHERIN 4.
 FT DOMAIN 495 616 CADHERIN 5.
 FT CARBOHYD 33 33 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 57 57 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 188 188 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 463 463 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 473 473 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 544 544 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CONFLICT 355 355 V -> D (IN REF. 2 AND 3).
 FT CONFLICT 647 647 H -> HQ (IN REF. 2 AND 3).
 SQ SEQUENCE 799 AA; 88253 MW; 98119B86039C6A0A CRC64;
 Query Match 8.1%; Score 89; DB 1; Length 799;
 Best Local Similarity 21.4%; Pred. No. 2.3;
 Matches 52; Conservative 34; Mismatches 91; Indels 66; Gaps 11;
 QY 13 HAEICQPGAENAFKVRLSIRLTALGDKAYAWDT-----NEEYLFKAMVAFSMRKVPN 63
 DB 432 HTDLERQFNINADGKTLATPLDRELSVWHNTIATIRNHSQISRPVPAIKVLDV-N 490
 QY 64 REATEIS---HVLIC-----NVTQVSFWVVTDPSSKNH-----TLPAVEVQSAIRMNK 109
 DB 491 DNAPEFASFEYAEFLCENGKPGQVITQVSA-MDKDDPKNGHYFLYSLPEMWNPNFTIKK 549
 QY 110 NRINNAPFL-----NDOTLEFLKIPSTLA---PPMDPSVPIWIIIPG----- 148
 DB 550 NEDNSLSILAKINGFNROKQEVLLPIIISDSGNPPLSSTLTIRVCGCSNDGVVQSCN 609
 QY 149 -----VIFCIIVAIALLILSGIWQRRRKNKEPSEVDDAEDKCNMIT 191
 DB 610 VEAYVLPIGLSMGALIAILACILLVIVLFP--VTLRRHKN-EPLIKDDEDVRENIIR 666
 QY 192 IEN 194
 DB 667 YDD 669
 RESULT 7
 CD44 MOUSE STANDARD; PRT; 778 AA.
 AC P15379; Q05732; Q61395; Q62060; Q62061; Q62062; Q62063; Q62408;
 AC Q62409; Q64296; Q99J14; Q9QX8;
 DT 01-APR-1990 (Rel. 14, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE CD44 antigen precursor (Phagocytic glycoprotein I) (PGP-1) (HUTCH-I)
 DE (Extracellular matrix receptor-III) (ECMR-III) (GP90 lymphocyte
 DE homing/adhesion receptor) (Hermes antigen) (Hyaluronate receptor)
 DE (LY-24).
 GN CD44.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORMS 4; 6; 7 AND 12).
 RC STRAIN=DRA/2; TISSUE=Lung;
 RX MEDLINE=93107170; PubMed=1469058;
 RA He Q., Lesley J., Hyman R., Ishihara K., Kincade P.W.;
 RT "Molecular isoforms of murine CD44 and evidence that the membrane
 RT proximal domain is not critical for hyaluronate recognition.";
 RL J. Cell Biol. 119:1711-1719(1992).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM 13).

RX MEDLINE=90038499; PubMed=2681416;
RA Zhou D.F.H., Ding J.F., Picker L.J., Bargatzke R.F., Butcher E.C.,
RA Goeddel D.V.;
RT "Molecular cloning and expression of Pgp-1. The mouse homolog of the
RT human H-CAM (Hermes) lymphocyte homing receptor.";
RL J. Immunol. 143:3390-3395(1989).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 13).
RX MEDLINE=90046829; PubMed=2682651;
RA Nottenburg C., Rees G., St John T.;
RA "Isolation of mouse CD44 cDNA: structural features are distinct from
RT the primate cDNA.";
RL Proc. Natl. Acad. Sci. U.S.A. 86:8521-8525(1989).
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RX MEDLINE=20318634; PubMed=10859330;
RA Wittig B.M., Johansson B., Zoeller M., Schwaerzler C., Guenther U.;
RA "Abrogation of experimental colitis correlates with increased
RT apoptosis in mice deficient for CD44 variant exon 7 (CD44v7).";
RL J. Exp. Med. 191:2053-2064(2000).
RN [5]
RP SEQUENCE FROM N.A. (ISOFORM 13).
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnorch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [6]
RP SEQUENCE FROM N.A. (ISOFORM 13).
RC STRAIN=C57BL/6J; TISSUE=Embryo;
RX MEDLINE=22354683; PubMed=12466851;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA Dalla E., Dragani T.A., Fletcher C.P., Forrest A., Frazer K.S.,
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Numata K., Okido T., Pavan W.J., Perte G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Saldelin A., Schneider C., Sempole C.A., Setou M., Shimada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Verardo R., Wagner L., Wahlstedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.;

RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [7]
RP SEQUENCE OF 8-778 FROM N.A. (ISOFORM 13).
RX MEDLINE=90094420; PubMed=2403559;
RA Wolffe E.J., Gause W.C., Pelfrey C.M., Holland S.M., Steinberg A.D.,
RA August J.T.;
RT "The cDNA sequence of mouse Pgp-1 and homology to human CD44 cell
RT surface antigen and proteoglycan core/link proteins.";
RL J. Biol. Chem. 265:341-347(1990).
RN [8]
RP SEQUENCE OF 224-637 FROM N.A. (ISOFORMS 1; 2; 3; 4; 5; 6; 7 AND 8).
RC STRAIN=GR;
RX MEDLINE=93219085; PubMed=8464707;
RA Toelg C., Hofmann M., Herrlich P., Ponta H.;
RT "Splicing choice from ten variant exons establishes CD44
RT variability.";
RL Nucleic Acids Res. 21:1225-1229(1993).
RN [9]
RP SEQUENCE OF 224-637 FROM N.A. (ISOFORM 9).
RC STRAIN=BALB/c;
RX MEDLINE=93286043; PubMed=8509359;
RA Screaton G.R., Bell M.V., Bell J.I., Jackson D.G.;
RT "The identification of a new alternative exon with highly restricted
RT tissue expression in transcripts encoding the mouse Pgp-1 (CD44)
RT homing receptor. Comparison of all 10 variable exons between mouse,
RT human, and rat.";
RL J. Biol. Chem. 268:12235-12238(1993).
RN [10]
RP PARTIAL SEQUENCE FROM N.A. (ISOFORMS 10 AND 11).
RC STRAIN=Swiss Webster;
RX MEDLINE=96355396; PubMed=8702806;
RA Yu Q., Toole B.P.;
RT "A new alternatively spliced exon between v9 and v10 provides a
RT molecular basis for synthesis of soluble CD44.";
RL J. Biol. Chem. 271:20603-20607(1996).
CC -!- FUNCTION: Main cell surface receptor for hyaluronate. Adhesion to
CC mucosal high endothelial venule and to types I and VI collagen.
CC Probably involved in matrix adhesion, lymphocyte activation and
CC lymph node homing.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=13;
CC Name=1;
CC IsoId=P15379-14; Sequence=Displayed;
CC Name=2;
CC IsoId=P15379-7; Sequence=VSP_007329;
CC Name=3;
CC IsoId=P15379-8; Sequence=VSP_007330;
CC Name=4; Synonyms=M2;
CC IsoId=P15379-4; Sequence=VSP_007331;
CC Name=5;
CC IsoId=P15379-9; Sequence=VSP_007332;
CC Name=6; Synonyms=M3;
CC IsoId=P15379-5; Sequence=VSP_005326;
CC Name=7; Synonyms=M4;
CC IsoId=P15379-6; Sequence=VSP_005327;
CC Name=8;
CC IsoId=P15379-10; Sequence=VSP_007330, VSP_007334;
CC Name=9;
CC IsoId=P15379-11; Sequence=VSP_007332, VSP_007335;
CC Name=10;
CC IsoId=P15379-12; Sequence=VSP_007336, VSP_007337;
CC Name=11;
CC IsoId=P15379-13; Sequence=VSP_007338, VSP_007339;
CC Name=12; Synonyms=M1;
CC IsoId=P15379-3; Sequence=VSP_005328;
CC Name=13; Synonyms=M0;
CC IsoId=P15379-2; Sequence=VSP_005329;
CC -!- PTM: N-glycosylated (By similarity).
CC -!- PTM: O-glycosylated; contains chondroitin sulfate glycans which
CC can be more or less sulfated (By similarity).

CC -!- PTM: Phosphorylated; activation of PKC results in the
CC dephosphorylation of Ser-742 (constitutive phosphorylation site),
CC and the phosphorylation of Ser-708 (By similarity).
CC -!- POLYMORPHISM: Two allelic forms of this glycoprotein, PGP-1.1 and
CC PGP-1.2, have been reported. The expressed product is PGP-1.1 (Ly-
CC 24.1).
CC -!- SIMILARITY: Contains 1 link domain.
CC -----
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CC -----
DR EMBL; X66084; CAA46883.1; -
DR EMBL; X66083; CAA46882.1; -
DR EMBL; X66082; CAA46881.1; -
DR EMBL; X66081; CAA46880.1; -
DR EMBL; M30655; AAA39922.1; -
DR EMBL; M27129; AAA37406.1; -
DR EMBL; M27130; AAA37407.1; -
DR EMBL; AJ251594; CAB61888.1; -
DR EMBL; BC005676; AAH05676.1; -
DR EMBL; AK045226; BAC32269.1; -
DR EMBL; J05163; AAA39923.1; -
DR EMBL; X69724; CAA49380.1; -
DR EMBL; L13611; AAA37145.1; -

Query Match 8.0%; Score 88; DB 1; Length 778;
Best Local Similarity 21.6%; Pred. No. 2.7;
Matches 24; Conservative 23; Mismatches 30; Indels 34; Gaps 3;

QY 128 IPSTLAPPMPDPSVPIWIIIFGVIFCIIVAIALLILSGIWQRRR----- 171
Db 671 VTTSGPMRRPQIPEWLIJ---LASLLALALILAVCIANRRRCGQKKLVINGNGTV 727
QY 172 KNKEPSEVDDAEDKCNMTIENGIPSD-----PLDMKGGI 207
Db 728 EDRKPSLNGEASKSQEMVHLVNKEPSETPDQMTADETRNLQSDVMKIGV 778

RESULT 8

CD44 CRIGR STANDARD; PRT; 362 AA.
AC P20944;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE CD44 antigen precursor (Phagocytic glycoprotein I) (PGP-1) (HUTCH-I)
DE (Extracellular matrix receptor-III) (ECMR-III) (GP90 lymphocyte
DE homing/adhesion receptor) (Hermes antigen) (Hyaluronate receptor).
GN CD44.
OS Cricetulus griseus (Chinese hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC Cricetulus.
OX NCBI_TaxID=10029;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90304889; PubMed=1694723;
RA Aruffo A., Stamenkovic I., Melnick M., Underhill C.B., Seed B.;
RT "CD44 is the principal cell surface receptor for hyaluronate.";
RL Cell 61:1303-1313(1990).
CC -!- FUNCTION: Main cell surface receptor for hyaluronate. Adhesion to
CC mucosal high endothelial venule and to types I and VI collagen.
CC Probably involved in matrix adhesion, lymphocyte activation and
CC lymph node homing.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- INDUCTION: By EBV.
CC -!- PTM: Extensively modified including N- and O-linked glycosylation,
CC addition of the glycosaminoglycan chondroitin sulfate, of sulfate,

CC of phosphate to cytoplasmic domain serine residues.
CC -!- SIMILARITY: Contains 1 link domain.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M33827; AAA36967.1; -
DR PIR; A35616; A35616.
DR HSSP; P98066; LTSG.
DR InterPro; IPR001231; CD44_antigen.
DR InterPro; IPR000538; Link.
DR Pfam; PF00193; Xlink; 1.
DR PRINTS; PR00658; CD44.
DR PRINTS; PR01265; LINKMODULE.
DR ProDom; PD000918; Link; 1.
DR SMART; SM00445; LINK; 1.
DR PROSITE; PS01241; LINK; 1.
KW Cell adhesion; Transmembrane; Glycoprotein; Phosphorylation; Receptor;
KW Proteoglycan; Signal; Alternative splicing;
KW Pyrrolidone carboxylic acid.
FT SIGNAL 1 22
FT CHAIN 23 362
FT DOMAIN 23 269
FT TRANSMEM 270 290
FT DOMAIN 291 362
FT DOMAIN 50 121
FT DOMAIN 152 160
FT DOMAIN 226 269
FT MOD_RES 23 23
FT DISULFID 55 120
FT DISULFID 79 99
FT MOD_RES 292 292
FT MOD_RES 326 326
FT CARBOHYD 27 27
FT CARBOHYD 59 59
FT CARBOHYD 102 102
FT CARBOHYD 112 112
FT CARBOHYD 122 122
FT CARBOHYD 174 174
FT CARBOHYD 256 256
SQ SEQUENCE 362 AA; 39775 MW; B89EB434E9EC948 CRC64;
Query Match 7.9%; Score 87; DB 1; Length 362;
Best Local Similarity 23.9%; Pred. No. 1.4;
Matches 26; Conservative 20; Mismatches 29; Indels 34; Gaps 3;
QY 130 STLAPPMPDPSVPIWIIIFGVIFCIIVAIALLILSGIWQRRR-----KN 173
Db 257 STSRPGGKPRVPEWLI---VLASLLALALILAVCIANRRRCGQKKLVINGNGKVED 313
QY 174 KEPSEVDDAEDKCNMTIENGIPSDP-----LDMKGGI 207
Db 314 RKPSELNGEASKSQEMVHLVNKEPSETPDQMTADETRNLQSDVMKIGV 362
RESULT 9
CD44 MESAU STANDARD; PRT; 431 AA.
AC Q60522; Q60523;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE CD44 antigen precursor (Phagocytic glycoprotein I) (PGP-1) (HUTCH-I)
DE (Extracellular matrix receptor-III) (ECMR-III) (GP90 lymphocyte
DE homing/adhesion receptor) (Hermes antigen) (Hyaluronate receptor)

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EMBL; M61875; AAAS3532.1; -
 DR EMBL; M61874; AAAS3534.1; -
 DR EMBL; U52179; AAA97915.1; -
 DR EMBL; U46957; AAA97920.1; -
 DR PIR; B38745; B38745.
 DR HSSP; P98066; 1TSG.
 DR InterPro; IPR001231; CD44_antigen.
 DR InterPro; IPR000538; Link.
 DR Pfam; PF00193; xlink; 1.
 DR PRINTS; PR00658; CD44.
 DR PRINTS; PR01265; LINKMODULE.
 DR ProDom; PD000918; Link; 1.
 DR SMART; SM00445; LINK; 1.
 DR PROSITE; PS01241; LINK; 1.

Cell adhesion; Transmembrane; Glycoprotein; Phosphorylation; Receptor; Proteoglycan; Signal; Alternative splicing; Pyrrolidone carboxylic acid.	1	21	CD44 ANTIGEN. EXTRACELLULAR (POTENTIAL). POTENTIAL. CYTOPLASMIC (POTENTIAL). LINK. ARG/LYS-RICH (BASIC). STEM. PYRROLIDONE CARBOXYLIC ACID (PROBABLE). BY SIMILARITY. BY SIMILARITY. PHOSPHORYLATION (BY PKC) (PARTIAL) (BY SIMILARITY). PHOSPHORYLATION (PARTIAL) (BY SIMILARITY).
SIGNAL	1	21	
CHAIN	22	503	
DOMAIN	22	410	
DOMAIN	411	431	
DOMAIN	432	503	
DOMAIN	51	123	
DOMAIN	154	162	
DOMAIN	228	410	
MOD_RES	22	22	
DISULFID	56	122	
DISULFID	80	100	
MOD_RES	433	433	
MOD_RES	467	467	
CARBOHYD	28	28	
CARBOHYD	60	60	
CARBOHYD	103	103	
CARBOHYD	114	114	
CARBOHYD	124	124	
CARBOHYD	266	266	
CARBOHYD	274	274	
CARBOHYD	306	306	
VARSPPLIC	224	385	
CONFLICT	74	74	
SEQUENCE	503 AA;	55945 MW;	FB489D009BD4EE22 CRC64;

RESULT 11
FLIF BACSU

FLIF BACSU STANDARD; PRT; 536 AA.

P23447;
01-NOV-1991 (Rel. 20, Created)
01-MAR-1992 (Rel. 21, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Flagellar M-ring protein.
FLIF OR BSU16210.
Bacillus subtilis.
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
NCBI_TaxID=1423;
[1]
SEQUENCE FROM N.A.
MEDLINE=91285431; PubMed=1905667;
Zuberi A.R., Ying C., Bischoff D.S., Ordal G.W.;
"Gene-protein relationships in the flagellar hook-basal body complex
of *Bacillus subtilis*: sequences of the flgB, flgC, flgG, flgE and
flf genes.";
Gene 101:23-31(1991).
[2]
SEQUENCE FROM N.A.
STRAIN=168;
MEDLINE=98044033; PubMed=9384377;
Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
Borriss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,
Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
Ghim S.-Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
Guiseppi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,
Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,
Kobayashi Y., Koetter P., Koningstein G., Krogh S., Kumano M.,
Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
Lee S.M., Levine A., Liu H., Masuda S., Mauel C., Medigue C.,
Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
Moore D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
Presecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y.,
Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
Sekiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S., Soldo B.,
Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K.,
Takeuchi M., Tamakoshi A., Tanaka T., Terpestra P., Tognoni A.,
Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,
Viari A., Wambutt R., Wedler B., Wedler H., Weitzneger T.,
Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
Yoshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.;
"The complete genome sequence of the Gram-positive bacterium *Bacillus
subtilis*.";
Nature 390:249-256(1997).
[3]
SEQUENCE OF 355-536 FROM N.A.
STRAIN=168;
MEDLINE=91258343; PubMed=1828465;
Albertini A.M., Caramori T., Crabb W.D., Scoffone F., Galizzi A.;
"The flag locus of *Bacillus subtilis* is part of a large operon coding
for flagellar structures, motility functions, and an ATPase-like
polypeptide.";
J. Bacteriol. 173:3573-3579(1991).
-!- FUNCTION: The M ring may be actively involved in energy
transduction.
-!- SUBUNIT: THE BASAL BODY CONSTITUTES A MAJOR PORTION OF THE
FLAGELLAR ORGANELLE AND CONSISTS OF FOUR RINGS (L,P,S, AND M)
MOUNTED ON A CENTRAL ROD. THE M RING IS INTEGRAL TO THE INNER
MEMBRANE OF THE CELL AND MAY BE CONNECTED TO THE FLAGELLAR ROD
VIA THE S RING. THE S (SUPRAMEMBRANE RING) LIES JUST DISTAL TO
THE M RING. THE L AND P RINGS LIE IN THE OUTER MEMBRANE AND THE
PERIPLASMIC SPACE, RESPECTIVELY.
-!- SUBCELLULAR LOCATION: Cytoplasmic; membrane-associated.
-!- SIMILARITY: Belongs to the flf family.

FT	CA_BIND	377	385	POTENTIAL.
FT	CA_BIND	441	449	POTENTIAL.
FT	SITE	437	439	CELL ATTACHMENT SITE (POTENTIAL).
FT	DISULFID	81	88	BY SIMILARITY.
FT	DISULFID	132	153	BY SIMILARITY.
FT	DISULFID	169	182	BY SIMILARITY.
FT	DISULFID	489	500	BY SIMILARITY.
FT	DISULFID	506	562	BY SIMILARITY.
FT	DISULFID	623	629	BY SIMILARITY.
FT	DISULFID	695	708	BY SIMILARITY.
FT	DISULFID	849	905	INTERCHAIN (BY SIMILARITY).
FT	DISULFID	910	915	BY SIMILARITY.
FT	CARBOHYD	66	66	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	104	104	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	159	159	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	221	221	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	284	284	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	293	293	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	486	486	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	587	587	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	701	701	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	719	719	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	751	751	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	762	762	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	818	818	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	877	877	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	904	904	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	952	952	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	986	986	N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ	SEQUENCE	1044 AA;	116141 MW;	3D59A318B51320CE CRC64;
Query Match 7.5%; Score 82.5; DB 1; Length 1044;				
Best Local Similarity 21.3%; Pred. No. 12;				
Matches 38; Conservative 28; Mismatches 59; Indels 53; Gaps 8;				
QY	17	CQPG-AENAFKVRLSIRLTALGDKAYAWDTNEEYLFKAWAFSMRKVPNREATISHVLLC	75	
Db	915	CNVGQLERKSAALKIRSLWAETFLQKNDPYTLSSNVSEFKVMPEYK	963	
QY	76	NVTQVSFWFVVTDPKSNHTLPAVEVQSAIRMNKNRINNAFFLNDQTLFLKIPSTLAPP	135	
Db	964	-----VQPAK---LP--EGSIAIRTS-----VIWST--PN	986	
QY	136	MDPSVPIWIIIFGVIFCIIVAIALLIL--SGIWQRKKNKEPSEVDDAEDKCNMIT	191	
Db	987	VSFVPLVWVILAILMGLLVLAVLTLALWKCGFFDRARPPQD--DMADREQLTNKTT	1042	
RESULT 14				
ITAH_HUMAN	STANDARD; PRT; 1189 AA.			
AC	Q9UKX5; Q9UKQ1;			
DT	16-OCT-2001 (Rel. 40, Created)			
DT	16-OCT-2001 (Rel. 40, Last sequence update)			
DT	28-FEB-2003 (Rel. 41, Last annotation update)			
DE	Integrin alpha-11 precursor.			
GN	ITGA11.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Fetal heart, and Osteoblast;			
RX	MEDLINE=99417678; PubMed=10486209;			
RA	Lehnert K., Ni J., Leung E., Gough S.M., Weaver A., Yao W.P., Liu D.,			
RA	Wang S.-X., Morris C.M., Krissansen G.W.;			
RT	"Cloning, sequence analysis, and chromosomal localization of the novel			
RT	human integrin alpha11 subunit (ITGA11).";			
RL	Genomics 60:179-187(1999).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Fetal muscle, and Uterus;			

RX	MEDLINE=99395147; PubMed=10464311;
RA	Velling T., Kuesche-Gullberg M., Sejersten T., Gullberg D.;
RT	"cDNA Cloning and Chromosomal Localization of Human alpha(11)
RT	Integrin. A collagen-binding, i domain-containing, beta(1)-associated
RT	integrin alpha-chain present in muscle tissues.";
RL	J. Biol. Chem. 274:25735-25742(1999).
RN	[3]
RP	SEQUENCE OF 954-1188 FROM N.A.
RC	TISSUE=Fibroblast;
RA	Andreu N., Estivill X., Escarceller M., Sumoy L.;
RL	Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
CC	-!- FUNCTION: INTEGRIN ALPHA-11/BETA-1 IS A RECEPTOR FOR COLLAGEN.
CC	-!- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA SUBUNIT. ALPHA-11
CC	ASSOCIATES WITH BETA-1.
CC	-!- SUBCELLULAR LOCATION: Type I membrane protein.
CC	-!- TISSUE SPECIFICITY: ACCORDING REF.2 HIGHEST LEVELS IN UTERUS AND
CC	HEART, INTERMEDIATE LEVELS IN SKELETAL MUSCLE AND INTERMEDIATE TO
CC	LOW LEVELS IN PANCREAS, KIDNEY AND PLACENTA. ACCORDING REF.1 ALSO
CC	FOUND IN BRAIN, COLON, LUNG, SMALL INTESTINE, STOMACH, TESTIS,
CC	SALIVARY GLANDS, THYROID GLANDS AND PROSTATE. VERY LOW LEVELS IN
CC	PERIPHERAL BLOOD LYMPHOCYTES, FETAL BRAIN AND FETAL LIVER.
CC	-!- DEVELOPMENTAL STAGE: STRONGLY UP-REGULATED IN DIFFERENTIATING
CC	FETAL MUSCLE CELLS (IN VITRO).
CC	-!- DOMAIN: THE INTEGRIN I-DOMAIN (INSERT) IS A VWFA DOMAIN. INTEGRINS
CC	WITH I-DOMAINS DO NOT UNDERGO PROTEASE CLEAVAGE.
CC	-!- SIMILARITY: Belongs to the integrin alpha chain family.
CC	-!- SIMILARITY: Contains 1 VWFA domain.
CC	-!- SIMILARITY: Contains 7 FG-GAP repeats.
CC	-----
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CC	or send an email to license@isb-sib.ch).
CC	-----
DR	EMBL; AF109681; AAP01258.1; --
DR	EMBL; AF137378; AAD51919.2; --
DR	EMBL; AL359064; CAB94392.1; --
DR	HSSP; P17301; LAOX.
DR	Genew; HGNC:6136; ITGA11.
DR	MIM; 604789; --
DR	GO; GO:0008305; C:integrin complex; TAS.
DR	GO; GO:0004895; F:cell adhesion receptor activity; TAS.
DR	GO; GO:0005518; F:collagen binding; TAS.
DR	GO; GO:0007160; P:cell-matrix adhesion; TAS.
DR	GO; GO:0007517; P:muscle development; TAS.
DR	InterPro; IPR000413; Integrin_alpha.
DR	InterPro; IPR002035; VWFA.
DR	Pfam; PF01839; FG-GAP; 3.
DR	Pfam; PF00092; vwa; 1.
DR	PRINTS; PR01185; INTEGRINA.
DR	PRINTS; PR00453; VWFADOMAIN.
DR	SMART; SM00191; Int_alpha; 5.
DR	SMART; SM00327; VWA; 1.
DR	PROSITE; PS00242; INTEGRIN_ALPHA; FALSE_NEG.
DR	PROSITE; PS50234; VWFA; 1.
KW	Integrin; Cell adhesion; Receptor; Glycoprotein; Transmembrane;
KW	Signal; Repeat; Calcium; Magnesium; Polymorphism.
FT	SIGNAL 1 22
FT	POTENTIAL.
FT	CHAIN 23 1189
FT	DOMAIN 23 1142
FT	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM 1143 1165
FT	POTENTIAL.
FT	DOMAIN 1166 1189
FT	CYTOPLASMIC (POTENTIAL).
FT	REPEAT 38 94
FT	FG-GAP 1.
FT	REPEAT 102 163
FT	FG-GAP 2.
FT	DOMAIN 167 345
FT	VWFA.
FT	REPEAT 359 420
FT	FG-GAP 3.
FT	REPEAT 422 475
FT	FG-GAP 4.
FT	REPEAT 477 537
FT	FG-GAP 5.
FT	REPEAT 539 598
FT	FG-GAP 6.
FT	REPEAT 601 653
FT	FG-GAP 7.

FT	DOMAIN	1154	1162	POLY-LEU.
FT	DOMAIN	1174	1177	POLY-ARG.
FT	CA_BIND	488	496	POTENTIAL.
FT	CA_BIND	551	559	POTENTIAL.
FT	CA_BIND	613	621	POTENTIAL.
FT	DISULFID	76	83	BY SIMILARITY.
FT	DISULFID	121	139	POTENTIAL.
FT	DISULFID	129	159	POTENTIAL.
FT	DISULFID	659	668	BY SIMILARITY.
FT	DISULFID	674	729	BY SIMILARITY.
FT	DISULFID	781	787	BY SIMILARITY.
FT	DISULFID	881	893	BY SIMILARITY.
FT	CARBOHYD	82	82	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	95	95	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	291	291	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	331	331	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	358	358	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	449	449	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	462	462	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	528	528	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	642	642	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	694	694	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	857	857	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	894	894	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	973	973	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	1032	1032	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	1040	1040	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	VARIANT	433	433	V -> M. /FTid=VAR_009889.
FT	VARIANT	524	524	R -> L. /FTid=VAR_009890.
FT	VARIANT	972	972	L -> P. /FTid=VAR_009891.
FT	VARIANT	1003	1003	I -> M. /FTid=VAR_009892.
FT	VARIANT	1030	1030	Missing. /FTid=VAR_009893.
FT	VARIANT	1094	1094	L -> V. /FTid=VAR_009894.
FT	SEQUENCE	1189 AA;	133609 MW;	60303C08A44CD52 CRC64;
Query Match 7.4%; Score 82; DB 1; Length 1189;				
Best Local Similarity 21.4%; Pred. No. 16;				
Matches 42; Conservative 40; Mismatches 74; Indels 40; Gaps 11;				
QY	7 FLVTAHAEQCQAENAFKVRISRTALGDK-----AYAWDTNREYLFKAMVAFSMRKV 61			
Db	998 FPIHGIMMKITPIATRSNRLKLRLDFTDEVANTSCNIWGNSTEYR-PTPVEEDLRA 1056			
QY	62 P-----NREATEISHVLLCNV-----TORVSP-----WFTVDPKSNHTLPVEVQS-AI 105			
Db	1057 POLNHSNSDVVSIN-----CNRLVPNQEINFHLGNLWL-----RSKALKYKSMKI 1104			
QY	106 RMN-----KNRINNAFFLNDQTLFLKIPSTLAPPMDPSVPIWIIIFGVIFCIIIVAIALLI 162			
Db	1105 MVNAALQRFHSPFIPRED-PSRQIVFEISKQEDMQVPIWIIIVGSTLGLLLALLVLA 1163			
QY	163 L--SGIWQRRRNKKEP 176			
Db	1164 LMKLGFRSARRRREP 1179			
RESULT 15				
LEU3 PHOLL				
ID	LEU3 PHOLL	STANDARD;	PRT;	363 AA.
AC	Q7N128;			
DT	15-MAR-2004 (Rel. 43, Created)			
DT	15-MAR-2004 (Rel. 43, Last sequence update)			
DT	15-MAR-2004 (Rel. 43, Last annotation update)			
DE	3-isopropylmalate dehydrogenase (EC 1.1.1.85) (Beta-IPM dehydrogenase)			
DE	(IMDH) (3-IPM-DH).			
GN	LEUB OR PLU3674.			
OS	Photorhabdus luminescens (subsp. laumondii).			

OC	Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC	Enterobacteriaceae; Photorhabdus.
OX	NCBI_TaxID=141679;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN=TT01;
RX	MEDLINE=22957627; PubMed=14528314;
RA	Duchaud E., Rusniok C., Frangeul L., Buchrieser C., Givaudan A.,
RA	Tacurit S., Bocs S., Boursaux-Eude C., Chandler M., Charles J.-F.,
RA	Dassa E., Derose R., Derzelle S., Freyssinet G., Gaudriault S.,
RA	Medigue C., Lanois A., Powell K., Siguier P., Vincent R., Wingate V.,
RA	Zouine M., Glaser P., Boemare N., Danchin A., Kunst F.;
RT	"The genome sequence of the entomopathogenic bacterium Photorhabdus
RT	luminescens.";
RL	Nat. Biotechnol. 21:1307-1313(2003).
CC	-!- FUNCTION: Catalyzes the oxidation of 3-carboxy-2-hydroxy-4-
CC	methylpentanoate (3-isopropylmalate) to 3-carboxy-4-methyl-2-
CC	oxopentanoate. The product decarboxylates to 4-methyl-2-
CC	oxopentanoate.
CC	-!- CATALYTIC ACTIVITY: 3-carboxy-2-hydroxy-4-methylpentanoate +
CC	NAD(+) = 3-carboxy-4-methyl-2-oxopentanoate + NADH.
CC	-!- PATHWAY: Leucine biosynthesis; third step.
CC	-!- SUBUNIT: Homodimer (By similarity).
CC	-!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC	-!- SIMILARITY: Belongs to the isocitrate and isopropylmalate
CC	dehydrogenases family. LeuB subfamily 1.
CC	-----
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CC	-----
DR	EMBL; BX571871; CAB16047.1; -.
DR	PhotoList; plu3674; -.
DR	HAWAP; MF_010333; -; 1.
DR	PROSITE; PS00470; IDH_IMDH; 1.
KW	Oxidoreductase; Leucine biosynthesis; NAD; Complete proteome.
SQ	SEQUENCE 363 AA; 39510 MW; 23126184A20FEABC CRC64;
Query Match 7.4%; Score 81.5; DB 1; Length 363;	
Best Local Similarity 25.0%; Pred. No. 4.4;	
Matches 47; Conservative 24; Mismatches 54; Indels 63; Gaps 10;	
QY	32 RTALGDKAYAWDTNREYLFK---AMVAF-SMRKVPNREATEISHVLLCNVTQVSW-F 85
Db	152 REGQKYEAFDTEVYHFEIERIARIAFESARKRSNK---VTSIDKANVLQSSVLWRE 207
QY	86 VVTDPKSNHTLPAVEVQSARIMKNKRINNAFFLNDQTLFLKIPSTLAPPMDPSVPIWII 145
Db	208 VVTEIAKAY--PDVEI-----NHMYIDNATMLIKDPSQ----- 239
QY	146 IFGVIFCIIIVAIALLILSGIWQRRRNKEPSEVDDAEDKCNENMITIENG-IPSDPLDMK 204
Db	240 -FDVMLCSNIFG-----DILSDECA-MITGSMGMLPSASLNEK 275
QY	205 GGILMMP 212
Db	276 GFGLYEPA 283
Search completed: March 31, 2004, 12:05:46	
Job time : 20 secs	

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OM protein - protein search, using sw model

Run on: March 31, 2004, 12:02:39 ; Search time 46 Seconds
(without alignments)
1454.127 Million cell updates/sec

Title: US-09-989-724-387
Perfect score: 1102
Sequence: 1 MLWLLFVLVTAHAEELCPG.....ENGIPSDPLDMKGILMMP 212

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues
Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_25:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phase:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1073	97.4	222	4 Q9HBJ8	Q9hbj8 homo sapien
2	928	84.2	222	11 Q9ESG4	Q9esg4 mus musculu
3	921	83.6	222	11 Q9ESG3	Q9esg3 rattus norv
4	376	34.1	804	4 Q9UFZ6	Q9ufz6 homo sapien
5	376	34.1	805	4 Q9NRA7	Q9nra7 homo sapien
6	376	34.1	816	4 Q86WT0	Q86wt0 homo sapien
7	373	33.8	805	4 Q9BYF1	Q9byf1 homo sapien
8	361	32.8	805	11 Q8R0I0	Q8r0i0 mus musculu
9	357	32.4	265	11 Q9D836	Q9d836 mus musculu
10	357	32.4	798	11 Q99N71	Q99n71 mus musculu
11	100	9.1	1053	5 Q8IAQ8	Q8iaq8 plasmodium
12	97.5	8.8	1086	5 O18428	O18428 geodia cydo
13	96.5	8.8	543	11 Q8COH7	Q8coh7 mus musculu
14	96.5	8.8	1012	11 O70304	O70304 mus musculu
15	95.5	8.7	1406	13 Q9W6V5	Q9w6v5 gallus gall
16	93.5	8.5	929	5 Q9VR32	Q9vr32 drosophila

17	91.5	8.3	823	11 Q8CE84	Q8ce84 mus musculu
18	91.5	8.3	1188	11 Q7TQC3	Q7tcq3 mus musculu
19	90	8.2	716	11 Q8C449	Q8c449 mus musculu
20	90	8.2	754	11 Q8BRK4	Q8brk4 mus musculu
21	89.5	8.1	161	11 Q9WUP8	Q9wup8 rattus norv
22	89.5	8.1	244	10 Q9C6E1	Q9c6el arabadopsis
23	89.5	8.1	1188	5 O76326	O76326 drosophila
24	89	8.1	1054	5 Q9U6S1	Q9u6s1 strongyloce
25	88.5	8.0	656	12 Q9QU36	Q9qu36 ttv-like mi
26	88	8.0	580	11 Q80X37	Q80x37 mus musculu
27	87	7.9	498	11 Q9D001	Q9d001 mus musculu
28	87	7.9	716	11 Q8C375	Q8c375 mus musculu
29	87	7.9	1326	2 Q8GHJ4	Q8ghj4 aeromonas p
30	86.5	7.8	252	10 Q9FX00	Q9fx00 arabadopsis
31	86.5	7.8	956	5 Q9W4T9	Q9w4t9 drosophila
32	86.5	7.8	1063	16 Q8KCX0	Q8kcx0 chlorobium
33	86	7.8	364	11 O70509	O70509 rattus norv
34	86	7.8	780	11 O08779	O08779 rattus norv
35	85.5	7.8	667	10 Q9M3D7	Q9m3d7 arabadopsis
36	85.5	7.8	826	4 Q8IY15	Q8iy15 homo sapien
37	85.5	7.8	959	5 Q9N9Y9	Q9n9y9 drosophila
38	85.5	7.8	975	5 Q97174	Q97174 drosophila
39	85.5	7.8	1148	4 Q9H7S7	Q9h7s7 homo sapien
40	85.5	7.8	1488	4 Q9HCM3	Q9hcm3 homo sapien
41	84.5	7.7	252	10 Q9FGB3	Q9fgb3 arabadopsis
42	84.5	7.7	468	16 Q9JVK7	Q9jvk7 neisseria m
43	84.5	7.7	823	4 Q8WYI8	Q8wyi8 homo sapien
44	84.5	7.7	1033	13 O42598	O42598 xenopus lae
45	84.5	7.7	1112	5 O02344	O02344 caenorhabdi

ALIGNMENTS

RESULT 1

Q9HBJ8	PRELIMINARY;	PRT;	222	AA.
ID Q9HBJ8				
AC Q9HBJ8;				
DT 01-MAR-2001 (Tremblrel. 16, Created)				
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)				
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)				
DE Kidney-specific membrane protein NX-17 (Hypothetical protein) (NX17 protein).				
OS Homo sapiens (Human).				
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC Mammalia; Theria; Primates; Catarrhini; Homnidae; Homo.				
OX NCBI_TaxID=9606;				
RN [1]				
RP SEQUENCE FROM N.A.				
RX MEDLINE=21264468; PubMed=11278314;				
RA Zhang H., Wada J., Hida K., Tsuchiyama Y., Hiragushi K., Shikata K., Wang H., Lin S., Kanwar Y.S., Makino H.;				
RT "Collectrin, a Collecting Duct-specific Transmembrane Glycoprotein, Is a Novel Homolog of ACE2 and Is Developmentally Regulated in Embryonic Kidneys.";				
RL J. Biol. Chem. 276:17132-17139(2001).				
RN [2]				
RP SEQUENCE FROM N.A.				
RC TISSUE=Colon;				
RX MEDLINE=22388257; PubMed=12477932;				
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Kettaman M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,				

RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalska U., Smallos D.E., Schnierch A., Schein J.E., Jones S.J., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences."; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN	[3]
RP	SEQUENCE FROM N.A.
RC	TISSUE=Bone marrow, Colon, and Kidney;
RA	Strausberg R.;
RL	Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases.
DR	EMBL; AF229179; AACG09466.1; -
DR	EMBL; BC015099; AAH15099.1; -
DR	EMBL; BC014317; AAH14317.1; -
DR	EMBL; BC050606; AAH50606.1; -
KW	Hypothetical protein.
SQ	SEQUENCE 222 AA; 25235 MW; 52C0ED522134BD05 CRC64;

Query Match 97.4%; Score 1073; DB 4; Length 222;
 Best Local Similarity 100.0%; Pred. No. 2.7e-105;
 Matches 206; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy	1	MLWLLFVLVTAIHAELCPGAENAFKVRLSINTALGDKAYAWDTNEEYLFKAMVAFSMRK	60
Dd	1	MLWLLFVLVTAIHAELCPGAENAFKVRLSINTALGDKAYAWDTNEEYLFKAMVAFSMRK	60
Oy	61	VPNREATEISHVLLCNVTQRVSFWFVVTPDSKNHTLPAVEVQS AIRMKNKRINNAFFLND	120
Dd	61	VPNREATEISHVLLCNVTQRVSFWFVVTPDSKNHTLPAVEVQS AIRMKNKRINNAFFLND	120
Oy	121	QTLEFLKIPSTLAPPMDPSVPFIWIIFGVIFCIIIVAJALLISGIWQRRRNKEPSEVD	180
Dd	121	QTLEFLKIPSTLAPPMDPSVPFIWIIFGVIFCIIIVAJALLISGIWQRRRNKEPSEVD	180
Oy	181	DAEDKCENMITIENGIPSDPLDMKG	206
Dd	181	DAEDKCENMITIENGIPSDPLDMKG	206

RESULT 2			
Q9ESG4			
ID	Q9ESG4	PRELIMINARY;	PRT; 222 AA.
AC	Q9ESG4;		
DT	01-MAR-2001	(TREMBLrel. 16, Created)	
DT	01-MAR-2001	(TREMBLrel. 16, Last sequence update)	
DT	01-JUN-2003	(TREMBLrel. 24, Last annotation update)	
DE	Kidney-specific membrane protein NX-17 (0610008J07Rik protein).		
GN	NX17 OR 0610008J07RIK.		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
OX	NCBI_TaxId=10090;		
RN	{1}		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=ICR;		
RX	MEDLINE=99362608; PubMed=10432394;		
RA	Zhang H., Wada J., Kanwar Y.S., Tsuchiyama Y., Hiragushi K., Hida K.,		
RA	Shikata K., Makino H.;		
RT	"Screening for genes up-regulated in 5/6 nephrectomized mouse		
RT	kidney.";		
RL	Kidney Int. 56:549-558(1999).		
RN	{2}		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=CS7BL/6J; TISSUE=Kidney;		
RX	MEDLINE=21085660; PubMed=11217851;		
RA	Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,		
RA	Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,		
RA	Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,		
RA	Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,		
RA	Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,		
RA	Pleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,		
RA	Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,		

Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T., Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-P., Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L., Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohtsuki S., Hayashizaki Y.;
 Functional annotation of a full-length mouse cDNA collection.;
 Nature 409:685-690(2001).
 [3]
 SEQUENCE FROM N.A.
 STRAIN=FVB/N; TISSUE=Kidney;
 MEDLINE=22388257; PubMed=12477932;
 Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schat N.K., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.C., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Heiton E., Kettelman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J., Marra M.A.;
 "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";
 Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 [4]
 SEQUENCE FROM N.A.
 STRAIN=FVB/N; TISSUE=Kidney;
 Strausberg R.;
 Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
 EMBL; AF178085; AAG09306.1; -
 EMBL; AK002337; BAB22022.1; -
 EMBL; BC049912; AAH49912.1; -
 MGD; MGI:1926234; Nxl7.
 SEQUENCE 222 AA; 25070 MW; C07E732CE92935A9 CRC64;
 Query Match 84.2%; Score 928; DB 11; Length 222;
 Best Local Similarity 84.5%; Pred. No. 6e-90;
 Matches 174; Conservative 15; Mismatches 17; Indels 0; Gaps 0;
 QY 1 MLMLLFLVTAIHAEICQPGAENAFKVRLSIRALTALGDKAYAWDTNNEYLKAMVAFSMRK 60
 DB 1 MLWALFVLVTTIAELCHPDAENAFKVRLSIRAAALGDKAYVWDTDQEYLFRAWVAFSMRK 60
 QY 61 VPNREATEISHVLLCNVTQRVSFVFWVVTDPKNTHTLPAVEVQSAIRMNKRNINNAFLND 120
 DB 61 VPNREATEISHVLLCNVTQRVSFVFWVVTDPKNTHTLPAVEVQSAIRMNKRNINNAFLND 120
 QY 121 QTLEFLKIPSTLAPMPDPSVPWIIIFGVIFCIIIVAIALLLSGIWQRRRNKKEPSEVD 180
 DB 121 HTLEFLKIPSTLAPMPDPSVPWIIIFGVIFCIVTVAIALLVLSGIRQRRRNKKGPGVE 180
 QY 181 DAEDKCNMITIENGIPSDPLDMKGG 206
 DB 181 DAEDKCNMITIENGIPSDPLDMKGG 206
 RESULT 3
 Q9ESG3
 ID Q9ESG3
 AC Q9ESG3;
 PRELIMINARY; PRT; 222 AA.

01-MAR-2001 (TREMBlrel. 16, Created)
01-MAR-2001 (TREMBlrel. 16, Last sequence update)
01-MAR-2001 (TREMBlrel. 16, Last annotation update)
Kidney-specific membrane protein NX-17.
Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
[1]
SEQUENCE FROM N.A.
STRAIN=Sprague-Dawley;
MEDLINE=99362608; PubMed=10432394;
Zhang H., Wada J., Kanwar Y.S., Tsuchiyama Y., Hiragushi K., Hida K.,
Shikata K., Makino H.;
"Screening for genes up-regulated in 5/6 nephrectomized mouse
kidney.";
Kidney Int. 56:549-558(1999).
EMBL; AF178086; AAG09307.1; -.
SEQUENCE 222 AA; 25226 MW; 7F4B166AE344F855 CRC64;

Query Match 83.6%; Score 921; DB 11; Length 222;
Best Local Similarity 84.5%; Pred. No. 3.3e-89;
Matches 174; Conservative 13; Mismatches 19; Indels 0; Gaps 0;

QY 1 MLWLLFPLVTAHAELCQPGAENAFKVRLSIRITAGDKAYAWDTNTEYLFKAMVAFSMRK 60
Db 1 MLWALFPLVTTIHAELCRPDAENAFKVRLSIKALGDKAYVWDTDEEYLFAMVAFSMRK 60
QY 61 VPNREATEISHVLLCNVTQRVSVFVVTDPKNTLPAVEVQSAIRMNKRINNAPFLND 120
Db 61 VPNREGTEISHVLLCNVTQRVSVFVVTDPKNTLPAVEVQSAIRMNKRINNAPFLDD 120
QY 121 QTLEFLKIPSTLAPPMDPSVPINIIIFGVIFCIIVAIALLILSGIWQRRRNKKEPSEVD 180
Db 121 HTLEFLKIPSTLAPPMDPSVPVNIIVFGVIFCIIVAIALLVLSGIRQRRRNKKGPPGVE 180
QY 181 DAEDKCNMITIENGIPSDPLDMKGG 206
Db 181 DAEDKCNIIITIENGIPCDPLDMKRG 206

RESULT 4
Q9UFZ6 PRELIMINARY; PRT; 804 AA.
AC Q9UFZ6;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Hypothetical protein (Fragment).
GN DKFZP434A014.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
SEQUENCE FROM N.A.
RP TISSUE=Testis;
RA Wambutt R., Heubner D., Mewes H.W., Gassenhuber J., Wiemann S.;
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL110224; CAB53682.1; -.
DR PIR; T14762; T14762.
DR MEROPS; M02.006; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004246; P:peptidyl-dipeptidase A activity; IEA.
DR GO; GO:0008270; F:zinc ion binding; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR001548; Peptidase M2.
DR InterPro; IPR006025; Pept M Zn_BS.
DR Pfam; PF01401; Peptidase M2; 1.
DR PRINTS; PR00791; PEPDIPASEA.
DR ProDom; PD004184; Peptidase M2; 1.
DR PROSITE; PS00142; ZINC_PROTEASE; 1.
KW Hypothetical protein.

SQ SEQUENCE 805 AA; 92462 MW; 8EE6E0A93155088 CRC64;

Query Match 34.1%; Score 376; DB 4; Length 805;
Best Local Similarity 47.9%; Pred. No. 8.2e-31;
Matches 79; Conservative 32; Mismatches 48; Indels 6; Gaps 3;

QY 19 PGAENAFKVRLSIRLTALGDKAYAWDTNEEYLFKAMVAFSMR----KVPNREAT-EISHVL 73
Db 612 PYADQSIKVRISLKSALGDKAYEWNDNEWYLFSSVAYAMRQYFLKVKQNMILFGEEDVR 671

QY 74 LCNVTQVSVFWVVDPSK-NHTLPAVEVQSAIRMNKNRINNNAFFLNDQTLFLKIPSTL 132
Db 672 VANLKPRISFNFFVTAPKNVSDIIPRTEVEKAIRMSRSRINDAFRLNDSLEFLGIQPTL 731

QY 133 APPMDPSVPIWIIIFGVIFCIIIVAIALLILSGIWQRRKNKPS 177
Db 732 GPPNQPPVSIWLVFGVMGVIVGIVILFTGIRDKKNKARS 776

RESULT 6

Q86WT0 PRELIMINARY; PRT; 816 AA.

Q86WT0; Q86WT0;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, last annotation update)
DE Similar to angiotensin I converting enzyme (Peptidyl-dipeptidase A) 2
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-Testis;
RA Strausberg R.;
RL Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
DR EMBL; BC048094; AAH48094.1; -
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004246; F:peptidyl-dipeptidase A activity; IEA.
DR GO; GO:0008270; F:zinc ion binding; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR001548; Peptidase M2.
DR InterPro; IPR006025; Pept M Zn BS.
DR Pfam; PF01401; Peptidase M2; 1.
DR PRINTS; PR00791; PEPDIPTASEA.
DR ProDom; PD004184; Peptidase M2; 1.
DR PROSITE; PS00142; ZINC_PROTEASE; 1.
FT NON_TER 1
SQ SEQUENCE 816 AA; 93516 MW; EF8BD58B3DA2EDF3 CRC64;

Query Match 34.1%; Score 376; DB 4; Length 816;
Best Local Similarity 47.9%; Pred. No. 8.3e-31;
Matches 79; Conservative 32; Mismatches 48; Indels 6; Gaps 3;

QY 19 PGAENAFKVRLSIRLTALGDKAYAWDTNEEYLFKAMVAFSMR----KVPNREAT-EISHVL 73
Db 623 PYADQSIKVRISLKSALGDKAYEWNDNEWYLFSSVAYAMRQYFLKVKQNMILFGEEDVR 682

QY 74 LCNVTQVSVFWVVDPSK-NHTLPAVEVQSAIRMNKNRINNNAFFLNDQTLFLKIPSTL 132
Db 683 VANLKPRISFNFFVTAPKNVSDIIPRTEVEKAIRMSRSRINDAFRLNDSLEFLGIQPTL 742

QY 133 APPMDPSVPIWIIIFGVIFCIIIVAIALLILSGIWQRRKNKPS 177
Db 743 GPPNQPPVSIWLVFGVMGVIVGIVILFTGIRDKKNKARS 787

RESULT 7

Q9BYF1 PRELIMINARY; PRT; 805 AA.

ID Q9BYF1
AC Q9BYF1
DT 01-JUN-2001 (TrEMBLrel. 17, Created)

DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE ACE2.
GN ACE2.

OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Komatsu T., Suzuki Y., Sugano S.;
RL Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Suzuki Y., Watanabe M., Sugano S.;
RT *Cloning, expression analysis and chromosomal localization of a novel
RT ACE like enzyme.";
RT ACE like enzyme.";
RL Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AB046569; BAB40370.1; -
DR MEROPS; M02.006; -
DR Genew; HGNC:13557; ACE2.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004246; F:peptidyl-dipeptidase A activity; IEA.
DR GO; GO:0008270; F:zinc ion binding; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR001548; Peptidase M2.
DR InterPro; IPR006025; Pept M Zn BS.
DR Pfam; PF01401; Peptidase M2; 1.
DR PRINTS; PR00791; PEPDIPTASEA.
DR ProDom; PD004184; Peptidase M2; 1.
DR PROSITE; PS00142; ZINC_PROTEASE; 1.
SQ SEQUENCE 805 AA; 92491 MW; D2AAB4C27088EB72 CRC64;

Query Match 33.8%; Score 373; DB 4; Length 805;
Best Local Similarity 47.3%; Pred. No. 1.7e-30;
Matches 78; Conservative 33; Mismatches 48; Indels 6; Gaps 3;

QY 19 PGAENAFKVRLSIRLTALGDKAYAWDTNEEYLFKAMVAFSMR----KVPNREAT-EISHVL 73
Db 612 PYADQSIKVRISLKSALGDKAYEWNDNEWYLFSSVAYAMRQYFLKVKQNMILFGEEDVR 671

QY 74 LCNVTQVSVFWVVDPSK-NHTLPAVEVQSAIRMNKNRINNNAFFLNDQTLFLKIPSTL 132
Db 672 VANLKPRISFNFFVTAPKNVSDIIPRTEVEKAIRMSRSRINDAFRLNDSLEFLGIQPTL 731

QY 133 APPMDPSVPIWIIIFGVIFCIIIVAIALLILSGIWQRRKNKPS 177
Db 732 GPPNQPPVSIWLVFGVMGVIVGIVILFTGIRDKKNKARS 776

RESULT 8

Q8R010 PRELIMINARY; PRT; 805 AA.

ID Q8R010
AC Q8R010;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, last annotation update)
DE RIKEN cDNA 2010305L05 gene.
GN ACE2 OR 2010305L05RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RA Strausberg R.;
RL Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
DR EMBL; BC026801; AAH26801.1; -
DR MGD; MGI:1917258; Ace2.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004246; F:peptidyl-dipeptidase A activity; IEA.
DR GO; GO:0008270; F:zinc ion binding; IEA.

DR GO: 0006508; P: proteolysis and peptidolysis; IEA.
 DR InterPro: IPR001548; Peptidase M2.
 DR InterPro: IPR006025; Pept_M_Zn_BS.
 DR InterPro: IPR001680; WD40.
 DR Pfam: PF01401; Peptidase M2; 1.
 DR PRINTS: PR00791; PEPDIPTASRA.
 DR ProDom: PD004184; Peptidase M2; 1.
 DR PROSITE: PS00678; WD REPEATS 1; 1.
 DR PROSITE: PS00142; ZINC_PROTEASE; 1.
 SQ SEQUENCE 805 AA; 92367 MW; D8B883AAC966A8D9 CRC64;
 Query Match 32.8%; Score 361; DB 11; Length 805;
 Best Local Similarity 40.9%; Pred. No. 3.2e-29;
 Matches 81; Conservative 35; Mismatches 52; Indels 30; Gaps 5;
 QY 19 PGAENAFKVRISIRLTALGDKAYAWDTNNEEYLFKAMVAFSMRK-----VFNREATEI 69
 Db 612 PYADQSIKVRISLKSALGANAYETNNEMFLPRSSVAYAMRKYSIIKNQTVPFLE---- 667
 QY 70 SHVLLCNVTQVSFWFVVDPSK-NHTLPAVEVQSAIRMNKNRINNNAFFLNDQTLFLKI 128
 Db 668 EDVRVSDLKPRVSFYFFVTSPQNVSDVIPRSEVEDAIRMSGRINDVFGNDNSLEFLGI 727
 QY 129 PSTLAPPMDPSVPIWIIIFGVFCIIIVAIALLILSGIWRKKNKEPSEVDADKCN 188
 Db 728 HPTLEPPYQPPVTIWLIIIFGVVMAVVGIIILVTGIKGRKKNETKRE----- 777
 QY 189 MITIENGIPSPDLMDKGG 206
 Db 778 -----EN-PYDSMDIGKG 789
 RESULT 9
 Q9D836 PRELIMINARY; PRT; 265 AA.
 AC Q9D836;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Adult male small intestine cDNA, RIKEN full-length enriched library,
 DE clone: 2010305L05 product: ANIGOTENSIN-converting enzyme-related
 DE carboxypeptidase, full insert sequence (fragment).
 GN ACE2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Small intestine;
 RA Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
 RA Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
 RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
 RA Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
 RA Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
 RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
 RA Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,
 RA Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
 RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
 RA Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
 RA Muramatsu M., Hayashizaki Y.;
 RL Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Small intestine;
 RX MEDLINE=22354683; PubMed=12466851;
 RA The FANTOM Consortium,
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs";
 RL Nature 420:563-573(2002).
 RN [3]
 RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Small intestine;
 RX MEDLINE=21085660; PubMed=11217851;
 RA RIKEN FANTOM Consortium;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Small intestine;
 RX MEDLINE=99279253; PubMed=10349636;
 RA Carninci P., Hayashizaki Y.;
 RT "High-efficiency full-length cDNA cloning.";
 RL Meth. Enzymol. 303:19-44(1999).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Small intestine;
 RX MEDLINE=20499374; PubMed=11042159;
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
 RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to
 RT prepare full-length cDNA libraries for rapid discovery of new genes.";
 RL Genome Res. 10:1617-1630(2000).
 RN [6]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Small intestine;
 RX MEDLINE=20530913; PubMed=11076861;
 RA Shibata K., Itoh M., Aizawa K., Nagao S., Sasaki N., Carninci P.,
 RA Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwaki S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 RT sequencing pipeline with 384 multicapillary sequencer.";
 RL Genome Res. 10:1757-1771(2000).
 DR EMBL; AK008530; BAB25723.2; -.
 DR MGD; MGI:1917258; Ace2.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0004246; F:peptidyl-dipeptidase A activity; IEA.
 DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
 DR InterPro: IPR001548; Peptidase M2.
 DR Pfam; PF01401; Peptidase_M2; 1.
 PT NON TER 1
 SQ SEQUENCE 265 AA; 30078 MW; 2A02B2CE3817C76C CRC64;
 Query Match 32.4%; Score 357; DB 11; Length 265;
 Best Local Similarity 44.1%; Pred. No. 2.2e-29;
 Matches 75; Conservative 33; Mismatches 48; Indels 14; Gaps 3;
 QY 19 PGAENAFKVRISIRLTALGDKAYAWDTNNEEYLFKAMVAFSMRK-----VFNREATEI 69
 Db 72 PYADQSIKVRISLKSALGANAYETNNEMFLPRSSVAYAMRKYSIIKNQTVPFLE---- 127
 QY 70 SHVLLCNVTQVSFWFVVDPSK-NHTLPAVEVQSAIRMNKNRINNNAFFLNDQTLFLKI 128
 Db 128 EDVRVSDLKPRVSFYFFVTSPQNVSDVIPRSEVEDAIRMSGRINDVFGNDNSLEFLGI 187
 QY 129 PSTLAPPMDPSVPIWIIIFGVFCIIIVAIALLILSGIWRKKNKEPSE 178
 Db 188 HPTLEPPYQPPVTIWLIIIFGVVMAVVGIIILVTGIKGRKKNETKRE 237
 RESULT 10
 Q99N71 PRELIMINARY; PRT; 798 AA.
 ID Q99N71
 AC Q99N71;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Anigotensin-converting enzyme-related carboxypeptidase.
 GN 2010305L05RIK OR ACE2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: April 4, 2004, 00:52:44 ; Search time 2717 Seconds
(without alignments)
2330.063 Million cell updates/sec

Title: US-09-989-724-387
Perfect score: 1102
Sequence: 1 MWLLFPLVTAHAEACQPG.....ENGIPSDPLDMKGGILMMP 212

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+p2n.model -DEV=xlh
-Q=/cgn2_1/USPTO_spool/US09989724/runat_31032004_081141_13300/app_query.fasta_1.391
-DB=EST -QFMT=fastap -SUFFIX=rst -MINMATCH=0.1 -LOOPCL=0 -LOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US09989724@cgn_1_1_1906@runat_31032004_081141_13300 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rod:*
26: em_gss_pbg:*
27: em_gss_vrl:*
28: gb_gss1:*

29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1089	98.8	669	29	AY399636	AY399636 Homo sapi
2	1085.5	98.5	792	12	BG400845	BG400845 602464068
3	1081	98.1	870	12	BI760941	BI760941 603043142
4	1078	97.8	663	14	CB139945	CB139945 K-EST0193
5	1056	95.8	639	14	CB137859	CB137859 K-EST0190
6	1048	95.1	855	12	BG427247	BG427247 602494304
7	1039	94.3	866	12	BG429618	BG429618 602501304
8	1036	94.0	780	12	BG429174	BG429174 602498032
9	1033	93.7	791	12	BG400319	BG400319 602464526
10	1026	93.1	804	12	BG429705	BG429705 602493709
11	1024	92.9	859	12	BG427839	BG427839 602501524
12	1021	92.6	782	12	BG433974	BG433974 602497274
13	1012	91.8	808	12	BG399473	BG399473 602441206
14	1010	91.7	736	12	BG399402	BG399402 602441161
15	1001.5	90.9	850	12	BG430955	BG430955 602500255
16	996	90.4	607	14	CB125058	CB125058 K-EST0173
17	996	90.4	888	12	BG400513	BG400513 602464748
18	988	89.7	677	12	BG427745	BG427745 602497114
19	986	89.5	1081	12	BM811234	BM811234 AGENCOURT
20	980	88.9	978	12	BI762437	BI762437 603048828
21	967	87.7	678	12	BG429011	BG429011 602501924
22	945.5	85.8	602	12	BG432624	BG432624 602500789
23	932.5	84.6	801	12	BG428217	BG428217 602498872
24	931	84.5	669	29	AY399638	AY399638 Mus muscu
25	931	84.5	720	12	BI102475	BI102475 602889668
26	931	84.5	755	14	CB955052	CB955052 AGENCOURT
27	931	84.5	1210	11	AK002337	AK002337 Mus muscu
28	929.5	84.3	884	12	BG399975	BG399975 602442028
29	929	84.3	735	9	AV653898	AV653898 AV653898
30	928	84.2	656	12	BI143454	BI143454 602907630
31	926	84.0	793	12	BI103785	BI103785 602887878
32	923	83.8	797	12	BI101134	BI101134 602886818
33	919.5	83.4	724	14	CB599934	CB599934 AGENCOURT
34	919	83.4	874	14	CF550832	CF550832 AGENCOURT
35	905	82.1	981	10	BF784771	BF784771 602111117
36	904	82.0	842	12	BI101926	BI101926 602887622
37	904	82.0	1051	12	BG399950	BG399950 602442002
38	903	81.9	750	14	CB599563	CB599563 AGENCOURT
39	897	81.4	915	10	BF789250	BF789250 602105150
40	893	81.0	782	12	BG969864	BG969864 602838808
41	883	80.1	669	29	AY399637	AY399637 Pan trogl
42	879	79.8	765	9	AV652853	AV652853 AV652853
43	877	79.6	730	14	CD241570	CD241570 AGENCOURT
44	869	78.9	742	12	BG969794	BG969794 602838708
45	862	78.2	901	10	BF786687	BF786687 602111448

ALIGNMENTS

RESULT 1
AY399636
LOCUS
DEFINITION Homo sapiens HCM0290 gene, VIRTUAL TRANSCRIPT, partial sequence.
ACCESSION AY399636
VERSION AY399636.1 GI:39755625
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 669)

AY399636 669 bp DNA linear GSS 12-DEC-2003
Homo sapiens HCM0290 gene, VIRTUAL TRANSCRIPT, partial sequence.
genomic survey sequence.

AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.

TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios

JOURNAL Science 302 (5652), 1960-1963 (2003)

PUBMED 14671302

REFERENCE 2 (bases 1 to 669)

AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.

TITLE Direct Submission

JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA

COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment.

FEATURES Location/Qualifiers

source 1..669

gene /organism="Homo sapiens" /mol_type="genomic DNA" /db_xref="taxon:9606" <1..>669 /locus_tag="HCM0290"

ORIGIN

Alignment Scores:

Pred. No.: 7.69e-131 Length: 669

Score: 1089.00 Matches: 212

Percent Similarity: 99.53% Conservative: 0

Best Local Similarity: 99.53% Mismatches: 0

Query Match: 98.82% Indels: 1

DB: 29 Gaps: 0

US-09-989-724-387 (1-212) x AY399636 (1-669)

Qy 1 MetLeuTrpLeuPheLeuValThrAlaIleHisAlaGluLeuCysGlnProGly 20

Db 1 ATGTTGTGGCTGCTCTTTTCTGGTGACTGCCATTTCATGCTGAACCTGTCAACCCAGGT 60

Qy 21 AlaGluAsnAlaPheLysValArgLeuSerIleArgThrAlaLeuGlyAspLysAlaTyr 40

Db 61 GCAGAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 120

Qy 41 AlaTrpAspThrAsnGluGluTyrLeuPheLysAlaMetValAlaPheSerMetArgLys 60

Db 121 GCCTGGGATACCAATGAAGAAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAA 180

Qy 61 ValProAsnArgGluAlaThrGluIleSerHisValLeuLeuCysAsnValThrGlnArg 80

Db 181 GTTCCCAACAGAGAGCAACAGAAATTTCCCATGTCTTACTTTGGCAATGTAAACCCAGAG 240

Qy 81 ValSerPheTrpPheValThrAspProSerLysAsnHisThrLeuProAlaValGlu 100

Db 241 GTATCAATCTGTTTGTGGTTACAGACCCCTTCAAAAATCACACCCCTTCTGCTGTGAG 300

Qy 101 ValGlnSerAlaIleArgMetAsnLysAsnArgIleAsnAsnAlaPhePheLeuAsnAsp 120

Db 301 GTGCAATCAGCCCATAGAATGAACAGAACCGGATCAACAATGCCCTTCTTCTAAATGAC 360

Qy 121 GlnThrLeuGluPheLeuLysIleProSerThrLeuAlaProProMetAspProSerVal 140

Db 361 CAAACTCTGGAATTTTAAAAATCCCTTCCACACTTGCACCCACCCATGGACCCCATCTGTG 420

Qy 141 ProIleTrpIleIleIlePheGlyValIlePheCysIleIleIleValAlaIleAlaLeu 160

Db 421 CCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCAC 480

Qy 161 LeuIleLeuSerGlyIleTrpGlnArgArgLysAsnLysGluProSerGluValAsp 180

Db 481 CTGATTTTATCAGGGATCTGGCAACGTTAGAAGAAAGAACAAAGAACCATCTGAAGTGGAT 540

Qy 181 AspAlaGluAspLysCysGluAsnMetIleThrIleGluAsnGlyIleProSerAspPro 200

Db 541 GACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAATGGCATCCCTCTGTATCCC 600

Qy 201 LeuAspMetLysGly-GlyIleLeuMetMetProSer 212

Db 601 CTGGACATGAAGGAGGCGCATATTAAATGATGCCTTCA 637

RESULT 2

BG400845

LOCUS BG400845 792 bp mRNA linear EST 12-MAR-2001

DEFINITION 602464068P1 NIH_MGC_75 Homo sapiens cDNA clone IMAGE:4592296 5', mRNA sequence.

ACCESSION BG400845

VERSION BG400845.1 GI:13294293

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 792)

AUTHORS NIH-MGC http://mgi.nci.nih.gov/.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D. Email: cgapbs-re@mail.nih.gov Tissue Procurement: CLONTECH Laboratories, Inc. cDNA Library Prepared by: The I.M.A.G.E. Consortium (LLNL) cDNA Library Arrayed by: Incyte Genomics, Inc. DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LLCM1330 row: 9 column: 17 High quality sequence stop: 784.

FEATURES Location/Qualifiers

source 1..792

organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="IMAGE:4592296" /lab_host="DH10B (T1 phage-resistant)" /clone_lib="NIH_MGC_75" /note="Organ: kidney; Vector: pDNR-LIB (Clontech); Site_1: SfiI (ggcgccctcgcc); Site_2: SfiI (ggccattatggcc); 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGGCATTATGGCC-3' and 3' adaptor sequence: 5'-ATTCTAGAGCCGAGCGCCGACATG-dT(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.65 kb (range 0.5-4.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH_MGC Library."

ORIGIN

Alignment Scores:

Pred. No.: 2.8e-130 Length: 792

Score: 1085.50 Matches: 211

Percent Similarity: 99.06% Conservative: 0

Best Local Similarity: 99.06% Mismatches: 1

Query Match: 98.50% Indels: 1

DB: 12 Gaps: 1

US-09-989-724-387 (1-212) x BG400845 (1-792)

Qy 1 MetLeuTrpLeuPheLeuValThrAlaIleHisAlaGluLeuCysGlnProGly 20

Db 32 ATGTTGTGGCTGCTCTTTTCTGGTGACTGCCATTTCATGCTGAACCTGTCAACCCAGGT 91

Qy 21 AlaGluAsnAlaPheLysValArgLeuSerIleArgThrAlaLeuGlyAspLysAlaTyr 40

Db 92 GCAGAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 151

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QY 41 AlaTrpAspThrAsnGluGluTyrLeuPheLysAlaMetValAlaPheSerMetArgLys 60
Db 152 GCCTGGGATACCAATGAAGATACCTCTTCAAAGCGATGGTAGCTTCTCCATGAGAAA 211
QY 61 ValProAsnArgGluAlaThrGluLeuSerHisValLeuLeuCysAsnValThrGlnArg 80
Db 212 GTTCCCAACAGAGAAGCAACAGAAATTTCCCAATGCTACTATTTGCAATGTAAACCCAGAG 271
QY 81 ValSerPheTrpPheValValThrAspProSerLysAsnHisThrLeuProAlaValGlu 100
Db 272 GTATCATCTCTGGTTGTGTGTACAGACCTTCAAAAAATCACACCTTCTCTGCTGTGAG 331
QY 101 ValGlnSerAlaLeuArgMetAsnLysAsnArgLysAsnAlaPhePheLeuAsnAsp 120
Db 332 GTGCAATCAGCCATAAGAAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGAC 391
QY 121 GlnThrLeuGluPheLeuLysIleProSerThrLeuAlaProProMetAspProSerVal 140
Db 392 CAAACTCTGGAAATTTTAAAAATCCCTTCCACACTTGCACCCACCCATGGACCCCTCTGTG 451
QY 141 ProIleTrpIleIlePheGlyValIlePheCysIleIleIleValAlaIleAlaLeu 160
Db 452 CCCATCTGGATTATATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTA 511
QY 161 LeuIleLeuSerGlyIleTrpGlnArgArgArgLysAsnLysGluProSerGluValAsp 180
Db 512 CTGATTTTATCAGGGATCTGGCAACGTAGAGAAGAAACAAGAACCATCTGAAGTGGAT 571
QY 181 AspAlaGluAspLysCysGluAsnMetIleThrIleGluAsnGlyIleProSerAspPro 200
Db 572 GACGCTGAAGATAAGTGTGAACAATGATCACAATGAAATGGAATGGCATCCCTCTGATCCC 631
QY 201 LeuAspMetLysGly---GlyIleLeuMetMetProSer 212
Db 632 CTGGACATGAAGGAGCGGCATATTAATGATGCTTCA 670

RESULT 3
BI760941
LOCUS
DEFINITION
BI760941
BI760941.1 GI:15752519
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 870)
NIH-MGC http://mgi.nci.nih.gov/.
AUTHORS
National Institutes of Health, Mammalian Gene Collection. (MGC)
JOURNAL
Unpublished (1999)
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11458 row: c column: 11
High quality sequence stop: 844.
Location/Qualifiers
1. -870
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5183554"
/lab_host="DH10B"
/clone_lib="NIH MGC 116"
/note="Organ: pooled colon, kidney, stomach; Vector:
pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA
```

source anonymous pool of 3 colons, age 26 yo male, 49 yo female, 71 yo male colon; 46 yo male kidney, and pool of 2 stomachs, 62 yo male and 70 yo female. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.4 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 023. Note: this is a NIH_MGC Library."

ORIGIN

```
Alignment Scores:
Pred. No.: 1.24e-129 Length: 870
Score: 1081.00 Matches: 210
Percent Similarity: 99.53% Conservative: 1
Best Local Similarity: 99.06% Mismatches: 0
Query Match: 98.09% Indels: 1
DB: 12 Gaps: 0

US-09-989-724-387 (1-212) x BI760941 (1-870)

QY 2 LeuTrpLeuLeuPhePheLeuValThrAlaIleHisAlaGluLeuCysGlnProGlyAla 21
Db 11 GTGTGGCTGCTCTTTTCTGGTGACTGCCATTCATGTGAACCTCTGTCAACCCAGGTGCA 70
QY 22 GluAsnAlaPheLysValArgLeuSerIleArgThrAlaLeuGlyAspLysAlaIleAla 41
Db 71 GAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATATGCC 130
QY 42 TrpAspThrAsnGluGluTyrLeuPheLysAlaMetValAlaPheSerMetArgLysVal 61
Db 131 TGGGATACCAATGAAGATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAGTT 190
QY 62 ProAsnArgGluAlaThrGluIleSerHisValLeuLeuCysAsnValThrGlnArgVal 81
Db 191 CCCAACAGAGAGAACACAGAAATTTCCCATGCTCTTGTGCAATGTAAACCCAGAGGTA 250
QY 82 SerPheTrpPheValValThrAspProSerLysAsnHisThrLeuProAlaValGluVal 101
Db 251 TCATTTCTGGTTGTGTGTACAGACCTTCAAATAATACACCCCTTCTGTGTGAGGTG 310
QY 102 GlnSerAlaIleArgMetAsnLysAsnArgIleAsnAsnAlaPhePheLeuAsnAspGln 121
Db 311 CAATCAGCCATAAGAAATGAACAGAACCGGATCAACAATGCCTTCTTTCTAAATGACCAA 370
QY 122 ThrLeuGluPheLeuLysIleProSerThrLeuAlaProProMetAspProSerValPro 141
Db 371 ACTCTGGAATTTTAAAAATCCCTTCCACACTTGCACCCACCCATGGACCCCATCTGTGCC 430
QY 142 IleTrpIleIleIlePheGlyValIlePheCysIleIleIleValAlaIleAlaLeuLeu 161
Db 431 ATCTGGATTATATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTTGCACACTG 490
QY 162 IleLeuSerGlyIleTrpGlnArgArgLysAsnLysGluProSerGluValAspAsp 181
Db 491 ATTTTATCAGGATCTGGCAACGTAGAAGAAAGAAACAAGAACCACTCTGAAGTGGATGAC 550
QY 182 AlaGluAspLysCysGluAsnMetIleThrIleGluAsnGlyIleProSerAspProLeu 201
Db 551 GCTGAAGATAAGTGTGAATAACATGATCACAATTTGAATAATGGCATCCCTCTGTATCCCCTG 610
QY 202 AspMetLysGly-GlyIleLeuMetMetProSer 212
Db 611 GACATGAAGGGAGGCATATTAATGATGCCCTTCA 644
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RESULT 4

```
CB139945
LOCUS
DEFINITION
K-EST0193043 L4SNU368b1 Homo sapiens cDNA clone L4SNU368b1-5-H10
5', mRNA sequence.
ACCESSION
CB139945
VERSION
CB139945.1 GI:28113403
KEYWORDS
EST.
```

CB139945 663 bp mRNA linear EST 29-JAN-2003

SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 663)
AUTHORS Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
Kim,Y.S.

TITLE 21C Frontier Korean EST Project 2001
JOURNAL Unpublished (2002)
COMMENT Contact: Kim YS

Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsung@mail.kribb.re.kr
Plate: 5 row: H column: 10
High quality sequence stop: 663.

FEATURES

source

1. .663
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="L4SNU368s1-5-H10"
/sex="M"
/tissue_type="Liver"
/cell_type="Polygonal"
/cell_line="SNU-368"
/lab_host="Top10P"
/clone_lib="L4SNU368s1"
/note="Organ: Liver; Vector: pCNS-D2; Site 1: EcoRI;
Site 2: NotI; The poly (A)+ RNA was dephosphorylated with
bacterial alkaline phosphatase (BAP) and then decapped
with tabacco acid pyrophosphatase (TAP). The decapped
intact mRNA was ligated with DNA-RNA linker including
EcoRI site by treatment of T4 RNA ligase and the first
strand cDNA was synthesized from oligo dt-selected mRNA by
priming with dt-tailed vector. The dt-tailed vector was
adjusted to have about 60nt. The cDNA vector was
circularized with E. coli DNA ligase after digestion of
EcoRI which site is also included in vector. An RNA strand
converted to a DNA strand by Okayama-Berg method. The
obtained cDNA vectors were used for transformation of
competent cells E. coli Top10P' by electroporation method.
The cDNA libraries constructed by this method are
full-length enriched cDNA library. After analyzing and
sequencing about 2,000 - 3,000 colonies in original cDNA
library, the abundant cDNAs were selected and amplified by
PCR reaction using vector region primer including T7
promotor as 5' primer and N(dt)14 as 3' primer. The PCR
products were used as template for synthesis of
biotinylated single stranded RNA by in vitro transcription
reaction. The synthesized RNA probes were hybridized with
antisense single stranded cDNAs prepared from original
library and incubated with avidin-gel. After removing
DNA-RNA hybrids by centrifuge, the subtracted cDNA
libraries were constructed by transfection of the
remaining DNA into competent cells E. coli Top10P' with
electroporation method."

ORIGIN

Alignment Scores:
Pred. No.: 2,06e-129 Length: 663
Score: 1078.00 Matches: 210
Percent Similarity: 99.53% Conservative: 0
Best Local Similarity: 99.53% Mismatches: 0
Query Match: 97.82% Indels: 1
DB: 14 Gaps: 0

US-09-989-724-387 (1-212) x CB139945 (1-663)

QY 1 MetLeuTrpLeuPheLeuValThrAlaIleHisAlaGluLeuCysGlnProGly 20

Db 31 ATGTTGGCTGCTCTTTTCTGGTGACTGCCATTCACTGCTGAACCTCTGTCAACACGGT 90
QY 21 AlaGluAsnAlaPheLysValArgLeuSerIleArgThrAlaLeuGlyAspLysAlaTyr 40
Db 91 GCAGAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 150
QY 41 AlaTrpAspThrAsnGluGluTyrLeuPheLysAlaMetValAlaPheSerMetArgLys 60
Db 151 GCCTGGGATACCAATGAAGATACCTCTTCAAGCGATGGTAGCTTTCTCCATGAGAAA 210
QY 61 ValProAsnArgGluAlaThrGluIleSerHisValLeuLeuCysAsnValThrGlnArg 80
Db 211 GTTCCCAACAGAGAGCAACAGAAATTTCCCATGTCTTACTTTGCAATGTAAACCCAGAG 270
QY 81 ValSerPheTrpPheValValThrAspProSerLysAsnHisThrLeuProAlaValGlu 100
Db 271 GTATCATCTGTTGTTGTGTACAGACCTTCAAAAAATCACACCTTCTCTGCTGTTGAG 330
QY 101 ValGlnSerAlaIleArgMetAsnLysAsnArgIleAsnAsnAlaPheLeuAsnAsp 120
Db 331 GTGCAATCAGCCATAGAATGAACAGAACCCGGATCAACAATGCCTTCTTTCTAAATGAC 390
QY 121 GlnThrLeuGluPheLeuLysIleProSerThrLeuAlaProProMetAspProSerVal 140
Db 391 CAAACTCTGGAATTTTAAAAATCCCTTCCACACTTGCCACCACCCCATCTGTG 450
QY 141 ProfileTrpIleIleIlePheGlyValIlePheCysIleIleIleValAlaIleAlaLeu 160
Db 451 CCCATCTGGATTATTATATTGTTGTGTATATTGTCATCATCATAGTTTGCATTCACCTA 510
QY 161 LeuIleLeuSerGlyIleTrpGlnArgArgArgLysAsnLysGluProSerGluValAsp 180
Db 511 CTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACCAAGAACCATCTGAAGTGGAT 570
QY 181 AspAlaGluAspLysCysGluAsnMetIleThrIleGluAsnGlyIleProSerAspPro 200
Db 571 GACGCTGAAGATAAGTGTGAACACATGATCACAAATGAAATGGCATCCCTCTGATCCC 630
QY 201 LeuAspMetLysGly-GlyIleLeuMetMet 210
Db 631 CTGGACATGAAAGAGGGGCATATTATATGATG 661

RESULT 5

CB137859
LOCUS CB137859 639 bp mRNA linear EST 29-JAN-2003
DEFINITION K-EST0190636 L4SNU368s1 Homo sapiens cDNA clone L4SNU368s1-11-F08
5', mRNA sequence.

ACCESSION

CB137859

VERSION

CB137859.1 GI:28108763

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 639)

AUTHORS

Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
Kim,Y.S.

TITLE

21C Frontier Korean EST Project 2001

JOURNAL

Unpublished (2002)

COMMENT

Contact: Kim YS

Genome Research Center

Korea Research Institute of Bioscience & Biotechnology

52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea

Tel: +82-42-860-4470

Fax: +82-42-860-4409

Email: yongsung@mail.kribb.re.kr

Plate: 11 row: F column: 08

High quality sequence stop: 639.

Location/Qualifiers

1. .639

/organism="Homo sapiens"

/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="L4SNU368s1-11-F08"
/sex="M"
/tissue_type="Liver"
/cell_type="Polygonal"
/cell_line="SNU-368"
/lab_host="Top10F"
/clone_lib="L4SNU368s1"
/note="Organ: Liver; Vector: pCNS-D2; Site 1: EcoRI;
Site 2: NotI; The poly (A)+ RNA was dephosphorylated with
bacterial alkaline phosphatase (BAP) and then decapped
with tobacco acid pyrophosphatase (TAP). The decapped
intact mRNA was ligated with DNA-RNA linker including
EcoRI site by treatment of T4 RNA ligase and the first
strand cDNA was synthesized from oligo dT-selected mRNA by
priming with dT-tailed vector. The dT-tailed vector was
adjusted to have about 60nt. The cDNA vector was
circularized with E. coli DNA ligase after digestion of
EcoRI which site is also included in vector. An RNA strand
converted to a DNA strand by Okayama-Berg method. The
obtained cDNA vectors were used for transfection of
competent cells E. coli Top10F by electroporation method.
The cDNA libraries constructed by this method are
full-length enriched cDNA library. After analyzing and
sequencing about 2,000 - 3,000 colonies in original cDNA
library, the abundant cDNAs were selected and amplified by
PCR reaction using vector region primer including T7
promotor as 5' primer and N(dT)14 as 3' primer. The PCR
products were used as template for synthesis of
biotinylated single stranded RNA by in vitro transcription
reaction. The synthesized RNA probes were hybridized with
antisense single stranded cDNAs prepared from original
library and incubated with avidin-gel. After removing
DNA-RNA hybrids by centrifuge, the subtracted cDNA
libraries were constructed by transfection of the
remaining DNA into competent cells E. coli Top10F with
electroporation method."

ORIGIN

Alignment Scores:
Pred. No.: 1.44e-126 Length: 639
Score: 1056.00 Matches: 203
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 95.83% Indels: 0
DB: 14 Gaps: 0

US-09-989-724-387 (1-212) x CB137859 (1-639)

QY	1	MetLeuTrpLeuLeuPhePheLeuValThrAlaIleHisAlaGluLeuCysGlnProGly	20
DB	31	ATGTTGTGGTCTCTTTTCTGGTACTGCTGCACTCATGCTGAACCTGTGTAACACAGGT	90
QY	21	AlaGluAsnAlaPheLysValArgLeuSerIleArgThrAlaLeuGlyAspLysAlaTyr	40
DB	91	GCAGAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT	150
QY	41	AlaTrpAspThrAsnGluGluTyrLeuPheLysAlaMetValAlaPheSerMetArgLys	60
DB	151	GCCTGGGATACCAATGAAGAATACTCTTCAAGCGATGGTAGCTTCTCCATGAGAAA	210
QY	61	ValProAsnArgGluAlaThrGluIleSerHisValLeuLeuCysAsnValThrGlnArg	80
DB	211	GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCTCTACTTTGCAATGTAAACAGAG	270
QY	81	ValSerPheTrpPheValValThrAspProSerLysAsnHisThrLeuProAlaValGlu	100
DB	271	GTATCATTTCTGGTTGTGTACAGACCTTCAAAAATCACAACCTTCTGCTGTGTAG	330
QY	101	ValGlnSerAlaIleArgMetAsnLysAsnArgIleAsnAsnAlaPhePheLeuAsnAsp	120
DB	331	GTGCAATCAGCCATAAGAAATGAACAAGACCGGATCAACATGCCTTCTTCTTAAATGAC	390

QY	121	GlnThrLeuGluPheLeuLysIleProSerThrLeuAlaProMetAspProSerVal	140
DB	391	CAAACTCTGGAATTTTAAAAATCCCTTCCACACTTGCACACCCATGGACCATCTGTG	450
QY	141	ProIleTrpIleIlePheGlyValIlePheCysIleIleIleValAlaIleAlaLeu	160
DB	451	CCCATCTGGATTATTATATTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTA	510
QY	161	LeuIleLeuSerGlyIleTrpGlnArgArgLysAsnLysGluProSerGluValAsp	180
DB	511	CTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAAGTGGAT	570
QY	181	AspAlaGluAspLysCysGluAsnMetIleThrIleGluAsnGlyIleProSerAspPro	200
DB	571	GACGCTGAAGATAAGTGTGAAGAACATGATCACAATTGAAATGGCATCCCTCTGATCCC	630
QY	201	LeuAspMet	203
DB	631	CTGGACATG	639

RESULT 6

BG427247
LOCUS BG427247 855 bp mRNA linear EST 14-MAR-2001
DEFINITION 602494304F1 NIH_MGC_75 Homo sapiens cDNA clone IMAGE:4608048 5',
mRNA sequence.

ACCESSION BG427247
VERSION BG427247.1 GI:133333753
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 855)
AUTHORS NIH-MGC <http://mgi.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-re@mail.nih.gov
Tissue Procurement: CLONTECH Laboratories, Inc.
cDNA Library Preparation: CLONTECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLCM1349 row: h column: 01
High quality sequence stop: 735.

FEATURES

Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4608048"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NIH_MGC_75"
/note="Organ: kidney; Vector: pDNR-LIB (Clontech); Site 1:
SfiI (ggccgcctggcc); Site 2: SfiI (ggccattatggcc); 5' and
3' adaptors were used in cloning as follows: 5' adaptor
sequence: 5'-CAGGCCATTATGGCC-3' and 3' adaptor sequence:
5'-ATTCTAGAGCGCGGCGGCGGACATG-dT(30)BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size 1.65
kb (range 0.5-4.0 kb). 15/15 colonies contained inserts
by PCR. This library was enriched for full-length clones
and was constructed by Clontech Laboratories (Palo Alto,
CA). Note: this is a NIH_MGC Library."

ORIGIN

Alignment Scores:
Pred. No.: 2.41e-125 Length: 855
Score: 1048.00 Matches: 211
Percent Similarity: 98.60% Conservative: 0
Best Local Similarity: 98.60% Mismatches: 1


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QY 202 AspMetLysGly--GlyIleLeuMetMetProSer 212
||||| ||| ||||| ||||| ||||| |||||
Db 633 GACATGACGGCAGGCATATTATGATGGCTTCA 667

RESULT 8
BG429174
LOCUS BG429174 780 bp mRNA linear EST 14-MAR-2001
DEFINITION 602498032F1 NIH_MGC_75 Homo sapiens cDNA clone IMAGE:4612062 5',
mRNA sequence.
ACCESSION BG429174
VERSION BG429174.1 GI:13335680
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 780)
NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: CLONTECH Laboratories, Inc.
cDNA Library Preparation: CLONTECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1359 row: o column: 07
High quality sequence stop: 718.
FEATURES
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1. 780
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4612062"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NIH_MGC_75"
/note="Organ: Kidney; Vector: pDNR-LIB (Clontech); Site 1:
SfiI (ggccattatggcc); Site 2: SfiI (ggccattatggcc); 5' and
3' adaptors were used in cloning as follows: 5' adaptor
sequence: 5'-CACGCCATTATGGCC-3' and 3' adaptor sequence:
5'-ATTCTAGAGCGGCGGCGGCGCATG-dT(30)BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size 1.65
kb (range 0.5-4.0 kb). 15/15 colonies contained inserts
by PCR. This library was enriched for full-length clones
and was constructed by Clontech Laboratories (Palo Alto,
CA). Note: this is a NIH_MGC Library."

ORIGIN
Alignment Scores:
Pred. No.: 7.72e-124 Length: 780
Score: 1036.00 Matches: 202
Percent Similarity: 99.51% Conservative: 0
Best Local Similarity: 99.51% Mismatches: 0
Query Match: 94.01% Indels: 1
DB: 12 Gaps: 0

US-09-989-724-387 (1-212) x BG429174 (1-780)

QY 11 AlaIleHisAlaGluLeuCysGlnProGlyAlaGluAsnAlaPheLysValArgLeuSer 30
||||| ||||| ||||| ||||| ||||| |||||
Db 2 GCCATTTCATGCTGAACCTCTGTCAACACGAGTGCAGAAAATGCTTTAAAGTGAGACTTAGT 61

QY 31 IleArgThrAlaLeuGlyAspLysAlaTyrAlaTrpAspThrAsnGluGluTyrLeuPhe 50
||||| ||||| ||||| ||||| ||||| |||||
Db 62 ATCAGAACAGCTCTGGGAGATAAAGCATATGCTCTGGGATACCAATGAAGATACTCTTC 121

QY 51 LysAlaMetValAlaPheSerMetArgLysValProAsnArgGluAlaThrGluIleSer 70
||||| ||||| ||||| ||||| ||||| |||||
Db 122 AAAGCGATGGTAGCTTCTCCATGAGAAAAGTTCCCAACAGAGAAGCAACAGAAATTTC 181

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QY 71 HisValLeuLeuCysAsnValThrGlnArgValSerPheTrpPheValValThrAspPro 90
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Db 182 CATGTCCTACTTTTGCATATGTAACCCAGAGGGTATCATTTCTGGTTTGTGTACAGACCCT 241

QY 91 SerLysAsnHisThrLeuProAlaValGluValGlnSerAlaIleArgMetAsnLysAsn 110
||||| ||||| ||||| ||||| ||||| |||||
Db 242 TCAAAAATATCACACCCCTTCTCTGCTGTGTGAGGTGCAATCAGCCATAGAATGAACAAGAAC 301

QY 111 ArgIleAsnAsnAlaPhePheLeuAsnAspGlnThrLeuGluPheLeuLysIleProSer 130
||||| ||||| ||||| ||||| ||||| |||||
Db 302 CGGATCAACAAATGCCTTCTTTCTAAATGACCAACTCTGGAAATTTTAAAAAATCCCTTCC 361

QY 131 ThrLeuAlaProProMetAspProSerValProIleTrpIleIleIlePheGlyValIle 150
||||| ||||| ||||| ||||| ||||| |||||
Db 362 ACACTTGACCAACCCATGGACCCATCTGTGCCCATCTGGATTATTATATTGGTGTGATA 421

QY 151 PheCysIleIleIleValAlaIleAlaLeuLeuIleLeuSerGlyIleTrpGlnArgArg 170
||||| ||||| ||||| ||||| ||||| |||||
Db 422 TTTTGCAATCATCATAGTTGCAATTGCACTACTACTGATTTTATCAGGGATCTGGCAACGTAGA 481

QY 171 ArgLysAsnLysGluProSerGluValAspAlaGluAspLysCysGluAsnMetIle 190
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Db 482 AGAAAGAACAAAGAACCATCTGAAGTGGATGACGCTGAAGATAAGTGTGAANAACATGATC 541

QY 191 ThrIleGluAsnGlyIleProSerAspProLeuAspMetLysGly-GlyIleLeuMetMe 210
||||| ||||| ||||| ||||| ||||| |||||
Db 542 ACAATTGAAATGGCATCCCTCTGATCCCTTGGACATGAAGGGAGGGCATATTAAATGAT 601

QY 210 tProSer 212
|||||
Db 602 GCCTTCA 608

RESULT 9
BG400319
LOCUS BG400319 791 bp mRNA linear EST 12-MAR-2001
DEFINITION 602464526F1 NIH_MGC_75 Homo sapiens cDNA clone IMAGE:4592575 5',
mRNA sequence.
ACCESSION BG400319
VERSION BG400319.1 GI:13293767
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 791)
NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: CLONTECH Laboratories, Inc.
cDNA Library Preparation: CLONTECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1331 row: c column: 08
High quality sequence stop: 711.
FEATURES
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1. 791
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4592575"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NIH_MGC_75"
/note="Organ: Kidney; Vector: pDNR-LIB (Clontech); Site 1:
SfiI (ggccgctcgcc); Site 2: SfiI (ggccattatggcc); 5' and
3' adaptors were used in cloning as follows: 5' adaptor
sequence: 5'-CACGCCATTATGGCC-3' and 3' adaptor sequence:
5'-ATTCTAGAGCGGCGGCGGCGCATG-dT(30)BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size 1.65
kb (range 0.5-4.0 kb). 15/15 colonies contained inserts
by PCR. This library was enriched for full-length clones
and was constructed by Clontech Laboratories (Palo Alto,
CA). Note: this is a NIH_MGC Library."

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kb (range 0.5-4.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH_MGC Library."

ORIGIN

Alignment Scores:
Pred. No.: 1.94e-123 Length: 791
Score: 1033.00 Matches: 205
Percent Similarity: 99.03% Conservative: 0
Best Local Similarity: 99.03% Mismatches: 1
Query Match: 93.74% Indels: 2
DB: 12 Gaps: 0

US-09-989-724-387 (1-212) x BG400319 (1-791)

Qy 1 MetLeuTrpLeuLeuPhePheLeuValThrAlaIleHisAlaGluLeuCysGlnProGly 20
Db 31 ATGTTGGCTGCTCTTTTCTGGGACTGCCATTTCATGCTGAACCTCTGTCAACCCAGGT 90
Qy 21 AlaGluAsnAlaPheLysValArgLeuSerIleArgThrAlaLeuGluAspLysAlaTyr 40
Db 91 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 150
Qy 41 AlaTrpAspThrAsnGluTyrLeuPheLysAlaMetValAlaPheSerMetArgLys 60
Db 151 GCCTGGGATACCAATGAAGATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA 210
Qy 61 ValProAsnArgGluAlaThrGluIleSerHisValLeuLeuCysAsnValThrGlnArg 80
Db 211 GTTCCCAACAGAGAGCAACAGAAATTTCCCATGTCTACTTTTGCATGTAACCCAGAGG 270
Qy 81 ValSerPheTrpPheValValThrAspProSerLysAsnHisThrLeuProAlaValGlu 100
Db 271 GTATCAATCTGGTTTGTGGTTACAGACCTTCAAAAAATCACACCTTCTCTGCTGTTGAG 330
Qy 101 ValGlnSerAlaIleArgMetAsnLysAsnArgIleAsnAsnAlaPhePheLeuAsnAsp 120
Db 331 GTGCAATCAGCCCATAGAATGAACAGAACCGGATCAACAATGCCCTTCTTCTAAATGAC 390
Qy 121 GlnThrLeuGluPheLeuLysIleProSerThrLeuAlaProProMetAspProSerVal 140
Db 391 CAAACTCTGGAATTTTAAAAATCCCTTCCACACTTGCACACCCCATGGACCCCATCTGTG 450
Qy 141 ProIleTrpIleIleIle-PheGlyValIlePheCysIleIleIleValAlaIleAlaLe 160
Db 451 CCCATCTGGATTATTATATTTCGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACT 510
Qy 160 uLeuIleLeuSerGlyIleTrpGlnArgArgArgLysAsnLysGluProSerGluValAs 180
Db 511 ACTGAT-TTATCAGGGATCTGGCAACGTAGAAGAAGAAAGAAACAAAGAACCATCTGAAGTGA 569
Qy 180 pAspAlaGluAspLysCysGluAsnMetIleThrIleGluAsnGlyIleProSerAspPr 200
Db 570 TGACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCTCTGATCC 629
Qy 200 oLeuAspMetLysGlyGly 206
Db 630 CCTGGACATGAAGGGAGGG 648

RESULT 10
BG429705
LOCUS BG429705 804 bp mRNA linear EST 14-MAR-2001
DEFINITION 602493709f1 NIH_MGC_75 Homo sapiens cDNA clone IMAGE:4607499 5',
mRNA sequence.
ACCESSION BG429705
VERSION BG429705.1 GI:13336211
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 804)

AUTHORS
TITLE
JOURNAL
COMMENT

NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: CLONTECH Laboratories, Inc.
CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1348 row: a column: 04
High quality sequence stop: 731.
Location/Qualifiers
1. 804

FEATURES
source

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4607499"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NIH_MGC_75"
/note="Organ: kidney; Vector: pDNR-LIB (Clontech); Site_1:
SfiI (ggcgctcgcc); Site 2: SfiI (ggccattatggcc); 5' and
3' adaptors were used in cloning as follows: 5' adaptor
sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence:
5'-ATTCTAGAGCCGAGCGCCGACATG-dt(30)BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size 1.65
kb (range 0.5-4.0 kb). 15/15 colonies contained inserts
by PCR. This library was enriched for full-length clones
and was constructed by Clontech Laboratories (Palo Alto,
CA). Note: this is a NIH_MGC Library."

ORIGIN

Alignment Scores:
Pred. No.: 1.62e-122 Length: 804
Score: 1026.00 Matches: 206
Percent Similarity: 96.73% Conservative: 1
Best Local Similarity: 96.26% Mismatches: 5
Query Match: 93.10% Indels: 3
DB: 12 Gaps: 0

US-09-989-724-387 (1-212) x BG429705 (1-804)

Qy 1 MetLeuTrpLeuLeuPhePheLeuValThrAlaIleHisAlaGluLeuCysGlnProGly 20
Db 32 ATGTTGGCTGCTCTTTTCTGGTACTGCCATTTCATGCTGAACCTCTGTCAACCCAGGT 91
Qy 21 AlaGluAsnAlaPheLysValArgLeuSerIleArgThrAlaLeuGluAspLysAlaTyr 40
Db 92 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 151
Qy 41 AlaTrpAspThrAsnGluTyrLeuPheLysAlaMetValAlaPheSerMetArgLys 60
Db 152 GCCTGGGATACCAATGAAGATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA 211
Qy 61 ValProAsnArgGluAlaThrGluIleSerHisValLeuLeuCysAsnValThrGlnArg 80
Db 212 GTTCCCAACAGAGAGCAACAGAAATTTCCCATGTCTACTTTGCAATGTAAACCCAGAGG 271
Qy 81 ValSerPheTrpPheValValThrAspProSerLysAsnHisThrLeuProAlaValGlu 100
Db 272 GTATCAATCTGGTTTGTGGTTACAGACCTTCAAAAAATCACACCTTCTCTGCTGTTGAG 331
Qy 101 ValGlnSerAlaIleArgMetAsnLysAsnArgIleAsnAsnAlaPhePheLeuAsnAsp 120
Db 332 GTGCAATCAGCCCATAGAATGAACAGAACCGGATCAACAATGCCCTTCTTCTTAAATGAC 391
Qy 121 GlnThrLeuGluPheLeuLysIleProSerThrLeuAlaProProMetAspProSerVal 140
Db 392 CAAACTCTGGAATTTTAAAAATCCCTTCCACACTTGCACACCCCATGGACCCCATCTGTG 451
Qy 141 ProIleTrpIleIleIlePheGlyValIlePheCysIleIleValAlaIleAlaLeu 160

LOCUS BG399473 808 bp mRNA linear EST 12-MAR-2001
DEFINITION 602441206F1 NIH_MGC_75 Homo sapiens cDNA clone IMAGE:4557073 5',
mRNA sequence.
ACCESSION BG399473
VERSION BG399473.1 GI:13293021
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 808)
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: CLONTECH Laboratories, Inc.
cDNA Library Preparation: CLONTECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLCM1260 row: 1 column: 02
High quality sequence stop: 637.

ORIGIN

Alignment Scores:
Pred. No.: 6.98e-122 Length: 782
Score: 1021.00 Matches: 206
Percent Similarity: 97.22% Conservative: 4
Best Local Similarity: 95.37% Mismatches: 2
Query Match: 92.65% Indels: 4
DB: 12 Gaps: 0

US-09-989-724-387 (1-212) x BG433974 (1-782)

Qy 1 MetLeuTrpLeuPheLeuValThrAlaIleHisAlaGluLeuCysGlnProGly 20
Db 32 ATGTTGGCTGCTCTTTTCTGGTGACTGCCATTTCATGCTGAACCTCTGTCAACCAAGT 91
Qy 21 AlaGluAsnAlaPheLysValArgLeuSerIleArgThrAlaLeuGlyAspLysAlaTyr 40
Db 92 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGAGATAAGCATAT 151
Qy 41 AlaTirPaspThrAsnGluGluTyrLeuPheLysAlaMetValAlaPheSerMetArgLys 60
Db 152 GCCTGGATACCAATGAAGAATACCTCTTCAAAGCGATGCTAGCTTTCTCCATGAGAAA 211
Qy 61 ValProAsnArgGluAlaThrGluIleSerHisValLeuLeuCysAsnValThrGlnArg 80
Db 212 GTTCCCAACAGAGAGCAACAGAAATTTCCCATGTCTTCTTGTCAATGTAACCCAGAG 271
Qy 81 ValSerPheTrpPheValThrAspProSerLysAsnHisThrLeuProAlaValGlu 100
Db 272 GTATCAATCTGTTTGTGTGTACAGACCTTCAAAAATCACACCTTCTCTGTGTGAG 331
Qy 101 ValGlnSerAlaIleArgMetAsnLysAsnArgIleAsnAsnAlaPhePheLeuAsnAsp 120
Db 332 GTGCAATCAGCCATAGATGAACAAGACCGGATCAACAATGCCCTTCTTCTAAATGAC 391
Qy 121 GlnThrLeuGluPheLeuLysIleProSerThrLeuAlaProProMetAspProSerVal 140
Db 392 CAAACTCTGGAATTTTAAANAATCCCTTCCACACTTGGCATCACCCATGGACCCATCTGTG 451
Qy 141 ProIleTrpIleIleIlePheGlyValIlePheCysIleIleIleValAlaIleAlaLeu 160
Db 452 CCCATCTGGATTATTATATTGTTGATATTGTCATCATCATAGTTCGAATTGCACATA 511
Qy 161 LeuIleLeuSerGlyIleTrpGlnArgArgArgLysAsnLysGluProSerGluValAsp 180
Db 512 CTGATTTTATCAGGGATCTGGCAACGTTAGAGAAAGAACAAAGAACCAATCTGAATGGAT 571
Qy 181 AspAlaGluAsp-LysCysGluAsnMetIleThrIleGlu-AsnGlyIleProSerAsp- 199
Db 572 GACGCTGAAGATCAAGTGTGACACCATGATCACCATTGACAAATGGGATCCCCTCTGAGT 631
Qy 200 ProLeuAspMetLysGly-GlyIleLeuMetMetProSer 212
Db 632 CCCCTGGACATGAAGGAGGGGCATATTATATGATGCTTCA 671

RESULT 13
BG399473

FEATURES
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4557073"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NIH_MGC_75"
/note="Organ: kidney; Vector: pDNR-LIB (Clontech); Site 1:
SfiI (ggccgctcgcc); Site 2: SfiI (ggccattatggcc); 5' and
3' adaptors were used in cloning as follows: 5' adaptor
sequence: 5'-CACGCCATTATGGCC-3' and 3' adaptor sequence:
5'-ATTCTAGAGCGGCGGCGGCACATG-dt(30)BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size 1.65
kb (range 0.5-4.0 kb). 15/15 colonies contained inserts
by PCR. This library was enriched for full-length clones
and was constructed by Clontech Laboratories (Palo Alto,
CA). Note: this is a NIH_MGC Library."

ORIGIN

Alignment Scores:
Pred. No.: 1.09e-120 Length: 808
Score: 1012.00 Matches: 200
Percent Similarity: 96.23% Conservative: 4
Best Local Similarity: 94.34% Mismatches: 6
Query Match: 91.83% Indels: 2
DB: 12 Gaps: 0
US-09-989-724-387 (1-212) x BG399473 (1-808)
Qy 1 MetLeuTrpLeuPheLeuValThrAlaIleHisAlaGluLeuCysGlnProGly 20
Db 32 ATGTTGGCTGCTCTTTTCTGGTGACTGCCATTTCATGCTGAACCTCTGTCAACCAAGT 91
Qy 21 AlaGluAsnAlaPheLysValArgLeuSerIleArgThrAlaLeuGlyAspLysAlaTyr 40
Db 92 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGAGATAAGCATAT 151
Qy 41 AlaTirPaspThrAsnGluGluTyrLeuPheLysAlaMetValAlaPheSerMetArgLys 60
Db 152 GCCTGGATACCAATGAAGAATACCTCTTCAAAGCGATGCTAGCTTTCTCCATGAGAAA 211
Qy 61 ValProAsnArgGluAlaThrGluIleSerHisValLeuLeuCysAsnValThrGlnArg 80
Db 212 GTTCCCAACAGAGAGCAACAGAAATTTCCCATGTCTTCTTGTCAATGTAACCCAGAG 271
Qy 81 ValSerPheTrpPheValThrAspProSerLysAsnHisThrLeuProAlaValGlu 100

Db 272 GTATCATCTGTTTGTGGTTACAGACCCCTTCAAAAAATCACACCCCTTCTGCTGTTGAG 331

Qy 101 ValGlnSerAlaIleArgMetAsnLysAsnArgIleAsnAsnAlaPhePheLeuAsnAsp 120

Db 332 GTGCAATCAGCCATAAGATGAACAAGAACCGGATCAACAATGCCCTTCTTTCTAAATGAC 391

Qy 121 GlnThrLeuGluPheLeuLysIleProSerThrLeuAlaProProMetAspProSerVal 140

Db 392 CAAACTCTGGAAATTTTAAATAATCCCTTCCACACTTGCACCCACCCATGGACCATCTGTG 451

Qy 141 ProIleTrpIleIlePheGlyValIlePheCysIleIleIleValAlaIleAlaLeu 160

Db 452 CCCATCTGGATTATATATTGGTGTGATATTTGGCATCATCATAGTTGCAATTGCACTA 511

Qy 161 LeuIleLeuSerGlyIleTrpGlnArgArgArgLysLysGluProSerGluValAsp 180

Db 512 CTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACCAAGAACCATCTGAAGTGGAT 571

Qy 181 AspAlaGluAspLys-Cys-GluAsnMetIleThrIleGluAsnGlyIleProSerAsp 200

Db 572 GACGCTGAAGATAAGTTGTTGAAACATGATCCCAATCTGAAATGGGCTTCCCTCTGATC 631

Qy 200 roleuAspMetLysGlyIleLeuMetMet 210

Db 632 CCCTGGACCTGAAGAGGAGGGCCCTATTAAATG 663

RESULT 14

LOCUS BG399402

DEFINITION BG399402 736 bp mRNA linear EST 12-MAR-2001

ACCESSION BG399402.1 GI:13292850

VERSION BG399402.1

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

AUTHORS 1 (bases 1 to 736)

TITLE NIH-MGC <http://mgc.nci.nih.gov/>.

JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-re@mail.nih.gov
Tissue Procurement: CLONTECH Laboratories, Inc.
cDNA Library Preparation: The I.M.A.G.E. Consortium (LNL)
cDNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Plate: L1CM1260 row: i column: 16
High quality sequence stop: 661.
Location/Qualifiers

FEATURES

source 1..736

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:4557015"

/lab_host="DH10B (T1 phage-resistant)"

/clone_lib="NIH MGC 75"

/note="Organ: kidney; Vector: pDNR-LIB (Clontech); Site_1: SfiI (ggcgccctcgcc); Site_2: SfiI (ggcattatggcc); 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGCCATTATGGC-3' and 3' adaptor sequence: 5'-ATTCTAGAGCCGAGCGGCGCATG-dt(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.65 kb (range 0.5-4.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH_MGC Library."

ORIGIN

Alignment Scores:

Pred. No.: 1.73e-120 Length: 736

Score: 1010.00 Matches: 204

Percent Similarity: 98.09% Conservative: 1

Best Local Similarity: 97.61% Mismatches: 2

Query Match: 91.65% Indels: 3

DB: 12 Gaps: 0

US-09-989-724-387 (1-212) x BG399402 (1-736)

Qy 5 LeuPhePheLeuValThrAlaIleHisAlaGluLeuCysGlnProGlyAlaGluAsnAla 24

Db 4 CTCCTTTTCTGCTGACTGCCATTTCATGCTGAACCTCTGTCAACCCAGGTGCAGAAAATGCT 63

Qy 25 PheLysValArgLeuSerIleArgThrAlaLeuGlyAspLysAlaIleAlaTrpAspThr 44

Db 64 TTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATATGCTGGGATACC 123

Qy 45 AsnGluGluTyrLeuPheLysAlaMetValAlaPheSerMetArgLysValProAsnArg 64

Db 124 AATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAAGTTCCCAACAGA 183

Qy 65 GluAlaThrGluIleSerHisValLeuLeuCysAsnValThrGlnArgValSerPheTrp 84

Db 184 GAAGCAACAGAAATTTCCCATGTCTCTACTTTGCAATGTAACCCAGAGGGTATCATCTGG 243

Qy 85 PheValValThrAspProSerLysAsnHisThrLeuProAlaValGluValGlnSerAla 104

Db 244 TTTTGTGTTACAGACCTTCAAAAAATCACACCTTCTGCTGTTGAGGTGCAATCAGCC 303

Qy 105 IleArgMetAsnLysAsnArgIleAsnAsnAlaPhePheLeuAsnAspGlnThrLeuGlu 124

Db 304 ATAAGAATGAACAAGAACCGGATCAACAATGCCCTTCTTCTAAATGACCAAACTCTGGAA 363

Qy 125 PheLeuLysIleProSerThrLeuAlaProProMetAspProSerValProIleTrpIle 144

Db 364 TTTTAAAAATCCCTTCCACACTTGCACCCACCCATGGACCCATCTGTGCCCATCTGGATT 423

Qy 145 IleIlePheGlyValIlePheCysIleIleIleValAlaIleAlaLeuLeuIleLeuSer 164

Db 424 ATTATATTGGTGTGATATTTTGGCATCATCATAGTTGCAATTCACACTACTGATTTTATCA 483

Qy 165 GlyIleTrpGlnArgArg-LysAsnLysGluProSerGluValAspAlaGluAs 184

Db 484 GGGATCTGGCAACGTAGAAGAAAGAACCAAGAACCATCTGAAGTGGATGACGCTGAAGA 543

Qy 184 pLysCysGluAsnMetIleThrIle-GluAsnGlyIleProSerAspProLeuAspMetL 204

Db 544 TAAGTGTGAAAACATGATCACAATTTGAAAATGGCATCCCTCTGTATCCCTG-GACATGA 602

Qy 204 ysGlyGlyIleLeuMetMetPro 211

Db 603 GGGAGGCGCATATTAAATGATGCCT 625

RESULT 15

LOCUS BG430955

DEFINITION BG430955P1 NIH_MGC_75 Homo sapiens cDNA clone IMAGE:4613965 5', mRNA linear EST 14-MAR-2001

ACCESSION BG430955

VERSION BG430955.1 GI:13337461

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

AUTHORS 1 (bases 1 to 850)

TITLE NIH-MGC <http://mgc.nci.nih.gov/>.

JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-re@mail.nih.gov
Tissue Procurement: CLONTECH Laboratories, Inc.

cDNA Library Preparation: CLONTECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLCM1364 row: n column: 14
High quality sequence stop: 681.

FEATURES

source

Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4613965"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NIH_MGC_75"
/note="Organ: kidney; Vector: pDNR-LIB (Clontech); Site 1:
SfiI (ggccgctcgcc); Site 2: SfiI (ggccattatggcc); 5' and
3' adaptors were used in cloning as follows: 5' adaptor
sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence:
5'-ATTCTAGAGCGCGGCGGCACATG-dt(30)BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size 1.65
kb (range 0.5-4.0 kb). 15/15 colonies contained inserts
by PCR. This library was enriched for full-length clones
and was constructed by Clontech Laboratories (Palo Alto,
CA). Note: this is a NIH_MGC Library."

ORIGIN

Alignment Scores:
Pred. No.: 2.73e-119 Length: 850
Score: 1001.50 Matches: 206
Percent Similarity: 97.18% Conservative: 1
Best Local Similarity: 96.71% Mismatches: 5
Query Match: 90.88% Indels: 4
DB: 12 Gaps: 0

US-09-989-724-387 (1-212) x BG430955 (1-850)

Qy 1 MetLeuTrpLeuPhePheLeuValThrAlaIleHisAlaGluLeuCysGlnProGly 20
Db |||||
36 ATGTTGGTGCTCTCTTTTCTGGTGACTGCCATTTCATGCTGAACCTCTCTCAACCGGT 95
Qy 21 AlaGluAsnAlaPheLysValArgLeuSerIleArgThrAlaLeuGlyAspLysAlaTyr 40
Db |||||
96 GCAGAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGAGATAAAGCATAT 155
Qy 41 AlaTrpAspThrAsnGluGluTyrLeuPheLysAlaMetValAlaPheSerMetArgLys 60
Db |||||
156 GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGTGTAGCTTTCTCCATGAGAAA 215
Qy 61 ValProAsnArgGluAlaThrGluIleSerHisValLeuLeuCysAsnValThrGlnArg 80
Db |||||
216 GTTCCCAACAGAGAGACACAGAAATTTCCCATGTCTACTTTGCAATGTAAACCCAGAGG 275
Qy 81 ValSerPheTrpPheValValThrAspProSerLysAsnHisThrLeuProAlaValGlu 100
Db |||||
276 GTATCATTTCTGGTTTGTGGTTACAGACCCCTTCAAAAATCACACCCCTTCTCTGTGTGAG 335
Qy 101 ValGlnSerAlaIleArgMetAsnLysAsnArgIleAsnAsnAlaPhePheLeuAsnAsp 120
Db |||||
336 GTGCAATCAGCCATAAGATGAACAGAACCGGATCAACATGCCTTCTTTCTAATGAC 395
Qy 121 GlnThrLeuGluPheLeuLysIleProSerThrLeuAlaProProMetAspProSerVal 140
Db |||||
396 CAAACTCTGGAATTTTAAATATCCCTTCCACACTTGCACCCCATGGACCCATCTGTG 455
Qy 141 ProIleTrpIleIleIlePheGlyValIlePheCysIleIleIleValAlaIleAlaLeu 160
Db |||||
456 CCCATCTGGATTATTATATTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCAC 515
Qy 161 LeuIleLeuSerGlyIleTrpGlnArgArgArgLysAsnLysGluProSerGluValAsp 180
Db |||||
516 CTGATTTTATCAGGGATCTGGCAACGTAGAGAAAGAACAAAGAACCATCTGAAGTGGAT 575

Qy 181 AspAlaGluAspLysCysGluAsnMetIleThrIleGluAsnGlyIleProSerAspPro 200
Db |||||
576 GACGCTGAAGATAG-TGTGAAAACATGATCACAATTGAAAAATGGAT-CCCTCTGATCCC 633
Qy 201 LeuAspMetLysGly-GlyIleLeuMetMetProSer 212
Db |||||
634 TG-GACATGAAGGAGGCGCATATTACTGATGCCTTCA 669

Search completed: April 4, 2004, 04:03:02
Job time : 2727 secs